



SEQUENCE LISTING

<110> Wright, David A.
Voytas, Daniel F.

<120> PLANT RETROELEMENTS AND METHODS RELATED THERETO

<130> P-1065A

<140> 09/586,106

<141> 2000-06-02

<150> 60/087,125

<151> 1998-05-29

<150> 09/322,478

<151> 1999-05-28

<160> 190

<170> FastSEQ for Windows Version 4.0

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<211> 18

<212> DNA

<213> Glycine max

<400> 1

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18

<210> 2

<211> 18

<212> DNA

<213> Glycine max

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18

<210> 3

<211> 6

<212> DNA

<213> Glycine max

<400> 3

ttgggg

6

<210> 4

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 4

Met Ala Ser Arg Lys Arg Lys

1

5

<210> 5

<211> 1263

<212> DNA

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 5

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atccttccag	agaggaatgt	agagcttggg	ccagggatgt	ttgatgagtt	cctgcaggaa	180
ctccagaggc	tcagatggga	ccagggttctg	acccgacttc	cagagaagtg	gattgatggt	240
gctctggtga	aggagtttta	ctccaaccta	tatgatccag	aggaccacag	tccgaagttt	300
tggaagtgttc	gaggacaggt	tgtgagattt	gatgctgaga	cgattaatga	tttctctgac	360
accccggtca	tcttggcaga	gggagaggat	tatccagcct	actctcagta	cctcagcact	420
cctccagacc	atgatgccat	cctttccgct	ctgtgtactc	cagggggacg	atttggtctg	480
aatggtgata	gtgccccctg	gaagctgctg	cggaaggatc	tgatgacgct	cgcgagaca	540
tggaagtgtgc	tctcttattt	taaccttgca	ctgacttttc	acacttctga	tattaatggt	600
gacagggccc	gactcaatta	tggttggtg	atgaagatgg	acctggacgt	gggcagcctc	660
atcttctcttc	agatcagtc	gatcgcccag	tccatcactt	ccaggcttgg	gttcccagcg	720
ttgatcacaa	cactgtgtga	gattcagggg	gttgctctctg	ataccctgat	ttttgagtca	780
ctcagtcctg	tgatcaacct	tgcttacatt	aagaagaact	gctggaaccc	tgccgatcca	840
tctatcacat	ttcaggggac	cgccgcacg	cgcaccagag	cttcggcgctc	ggcatctgag	900
gctcctcttc	catcccagca	tccttctcag	cctttttccc	agagaccacg	gcctccactt	960
ctatccacct	cagcacctcc	atacatgcat	ggacagatgc	tcaggtcctt	gtaccagggg	1020
cagcagatca	tcattcagaa	cctgtatcga	ttgtccctac	atttgagat	ggatctgcc	1080
ctcatgactc	cggaggccta	tcgtcagcag	gtcgccaagc	taggagacca	gccctccact	1140
gacagggggg	aagagccttc	tggaagccgt	gctactgagg	atcctgccgt	tgatgaagac	1200
ctcatagctg	acttggctgg	cgctgattgg	agcccatggg	cagacttggg	cagaggcagc	1260
tga						1263

<210> 6

<211> 421

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 6

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Asn	Trp	Asp	Ser	Ser	Arg	Phe	Thr	Phe	Glu	Ile	Ala	Trp	His	Arg	Tyr
			20					25					30		
Gln	Asp	Ser	Ile	Gln	Leu	Arg	Asn	Ile	Leu	Pro	Glu	Arg	Asn	Val	Glu
		35				40					45				
Leu	Gly	Pro	Gly	Met	Phe	Asp	Glu	Phe	Leu	Gln	Glu	Leu	Gln	Arg	Leu
	50				55				60						
Arg	Trp	Asp	Gln	Val	Leu	Thr	Arg	Leu	Pro	Glu	Lys	Trp	Ile	Asp	Val
65				70				75					80		
Ala	Leu	Val	Lys	Glu	Phe	Tyr	Ser	Asn	Leu	Tyr	Asp	Pro	Glu	Asp	His
			85				90					95			
Ser	Pro	Lys	Phe	Trp	Ser	Val	Arg	Gly	Gln	Val	Val	Arg	Phe	Asp	Ala
		100					105						110		

Glu Thr Ile Asn Asp Phe Leu Asp Thr Pro Val Ile Leu Ala Glu Gly
 115 120 125
 Glu Asp Tyr Pro Ala Tyr Ser Gln Tyr Leu Ser Thr Pro Pro Asp His
 130 135 140
 Asp Ala Ile Leu Ser Ala Leu Cys Thr Pro Gly Gly Arg Phe Val Leu
 145 150 155 160
 Asn Val Asp Ser Ala Pro Trp Lys Leu Leu Arg Lys Asp Leu Met Thr
 165 170 175
 Leu Ala Gln Thr Trp Ser Val Leu Ser Tyr Phe Asn Leu Ala Leu Thr
 180 185 190
 Phe His Thr Ser Asp Ile Asn Val Asp Arg Ala Arg Leu Asn Tyr Gly
 195 200 205
 Leu Val Met Lys Met Asp Leu Asp Val Gly Ser Leu Ile Ser Leu Gln
 210 215 220
 Ile Ser Gln Ile Ala Gln Ser Ile Thr Ser Arg Leu Gly Phe Pro Ala
 225 230 235 240
 Leu Ile Thr Thr Leu Cys Glu Ile Gln Gly Val Val Ser Asp Thr Leu
 245 250 255
 Ile Phe Glu Ser Leu Ser Pro Val Ile Asn Leu Ala Tyr Ile Lys Lys
 260 265 270
 Asn Cys Trp Asn Pro Ala Asp Pro Ser Ile Thr Phe Gln Gly Thr Arg
 275 280 285
 Arg Thr Arg Thr Arg Ala Ser Ala Ser Ala Ser Glu Ala Pro Leu Pro
 290 295 300
 Ser Gln His Pro Ser Gln Pro Phe Ser Gln Arg Pro Arg Pro Pro Leu
 305 310 315 320
 Leu Ser Thr Ser Ala Pro Pro Tyr Met His Gly Gln Met Leu Arg Ser
 325 330 335
 Leu Tyr Gln Gly Gln Gln Ile Ile Ile Gln Asn Leu Tyr Arg Leu Ser
 340 345 350
 Leu His Leu Gln Met Asp Leu Pro Leu Met Thr Pro Glu Ala Tyr Arg
 355 360 365
 Gln Gln Val Ala Lys Leu Gly Asp Gln Pro Ser Thr Asp Arg Gly Glu
 370 375 380
 Glu Pro Ser Gly Ala Ala Thr Glu Asp Pro Ala Val Asp Glu Asp
 385 390 395 400
 Leu Ile Ala Asp Leu Ala Gly Ala Asp Trp Ser Pro Trp Ala Asp Leu
 405 410 415
 Gly Arg Gly Ser Glx
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<210> 7

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 7

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acctcacctc	ctccttctcc	aaattatgct	cagatggacg	gggaaccggc	acaaagagtc	180
acactagagg	acttctctaa	taccaccact	cctcagttct	ttacaagtat	cacaaggccg	240
gaagtccaag	cagatctcct	tactcaaggg	aacctcttcc	atggtcttcc	aaatgaagat	300
ccatatgcgc	atctagcctc	atacatagag	atatgcagca	ccgttaaaat	cgccggagtt	360
cctaaagatg	cgatactcct	taacctcttt	tccttttccc	tagcaggaga	ggcaaaaaga	420

tggttgact	cctttaagg	caatagctta	agaacatggg	aagaagtagt	ggaaaaattc	480
ttaaagaagt	atttcccaga	gtcaaagacc	gtcgaacgaa	agatggagat	ttcttatttc	540
catcaatttc	tggtatgaatc	ccttagcgaa	gcactagacc	atttccacgg	attgctaaga	600
aaaacaccaa	cacacagata	cagcgagcca	gtacaactaa	acatattcat	cgatgacttg	660
caactcttaa	tcgaaacagc	tactagaggg	aagatcaagc	tgaagactcc	cgaagaagcg	720
atggagctcg	tcgagaacat	ggcggctagc	gatcaagcaa	tccttcatga	tcacacttat	780
gttcccacaa	aaagaagcct	cttggagctt	agcacgcagg	acgcaacttt	ggtacaaaaac	840
aagctgttga	cgaggcagat	agaagccctc	atcgaaaccc	tcagcaagct	gcctcaacaa	900
ttacaagcga	taagttcttc	ccactcttct	gttttgagg	tagaagaatg	ccccacatgc	960
agagggacac	atgagcctgg	acaatgtgca	agccaacaag	acccctctcg	tgaagtaaat	1020
tatataggca	tactaaatcg	ttacggattt	cagggctaca	accagggaaa	tccatctgga	1080
ttcaatcaag	gggcaacaag	atttaatcac	gagccaccgg	ggtttaatca	aggaagaaac	1140
ttcatgcaag	gctcaagttg	gacgaataaa	ggaaatcaat	ataaggagca	aaggaaccaa	1200
ccaccatacc	agccaccata	ccagcaccct	agccaaggtc	cgaatcagca	agaaaagccc	1260
acaaaaatag	aggaactgct	gctgcaattc	atcaaggaga	caagatcaca	tcaaaaagagc	1320
acggatgcag	ccattcgga	tctagaagtt	caaattgggccc	aactggcgca	tgacaaagcc	1380
gaacggccca	ctagaacttt	cggtgctaac	atggagagaa	gaaccccaag	gaaggataaa	1440
gcagtactga	ctagagggga	gagaagagcg	caggagagg	gtaaggttga	aggagaagac	1500
tggccagaag	aaggaaggac	agagaagaca	gaagaagaag	agaagggtgc	agaagaacct	1560
aagcgtacca	agagccagag	agcaagggaa	gccaag			1596

<210> 8

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 8

Met	Arg	Gly	Arg	Thr	Ala	Ser	Gly	Asp	Val	Val	Pro	Ile	Asn	Leu	Glu
1				5				10						15	
Ile	Glu	Ala	Thr	Cys	Arg	Arg	Asn	Asn	Ala	Ala	Arg	Arg	Arg	Arg	Glu
			20					25					30		
Gln	Asp	Ile	Glu	Gly	Ser	Ser	Tyr	Thr	Ser	Pro	Pro	Pro	Ser	Pro	Asn
		35					40					45			
Tyr	Ala	Gln	Met	Asp	Gly	Glu	Pro	Ala	Gln	Arg	Val	Thr	Leu	Glu	Asp
	50					55				60					
Phe	Ser	Asn	Thr	Thr	Thr	Pro	Gln	Phe	Phe	Thr	Ser	Ile	Thr	Arg	Pro
65					70					75				80	
Glu	Val	Gln	Ala	Asp	Leu	Leu	Thr	Gln	Gly	Asn	Leu	Phe	His	Gly	Leu
				85					90					95	
Pro	Asn	Glu	Asp	Pro	Tyr	Ala	His	Leu	Ala	Ser	Tyr	Ile	Glu	Ile	Cys
		100						105					110		
Ser	Thr	Val	Lys	Ile	Ala	Gly	Val	Pro	Lys	Asp	Ala	Ile	Leu	Leu	Asn
	115						120					125			
Leu	Phe	Ser	Phe	Ser	Leu	Ala	Gly	Glu	Ala	Lys	Arg	Trp	Leu	His	Ser
	130					135					140				
Phe	Lys	Gly	Asn	Ser	Leu	Arg	Thr	Trp	Glu	Glu	Val	Val	Glu	Lys	Phe
145					150					155				160	
Leu	Lys	Lys	Tyr	Phe	Pro	Glu	Ser	Lys	Thr	Val	Glu	Arg	Lys	Met	Glu
			165					170						175	
Ile	Ser	Tyr	Phe	His	Gln	Phe	Leu	Asp	Glu	Ser	Leu	Ser	Glu	Ala	Leu
		180						185					190		
Asp	His	Phe	His	Gly	Leu	Leu	Arg	Lys	Thr	Pro	Thr	His	Arg	Tyr	Ser
	195						200					205			
Glu	Pro	Val	Gln	Leu	Asn	Ile	Phe	Ile	Asp	Asp	Leu	Gln	Leu	Leu	Ile

210		215		220
Glu Thr Ala Thr Arg Gly Lys Ile Lys Leu Lys Thr Pro Glu Glu Ala				
225		230		235
Met Glu Leu Val Glu Asn Met Ala Ala Ser Asp Gln Ala Ile Leu His				240
	245		250	255
Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr				
	260		265	270
Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu				
	275		280	285
Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile				
	290		295	300
Ser Ser Ser His Ser Ser Val Leu Gln Val Glu Glu Cys Pro Thr Cys				320
305		310		315
Arg Gly Thr His Glu Pro Gly Gln Cys Ala Ser Gln Gln Asp Pro Ser				335
	325		330	
Arg Glu Val Asn Tyr Ile Gly Ile Leu Asn Arg Tyr Gly Phe Gln Gly				
	340		345	350
Tyr Asn Gln Gly Asn Pro Ser Gly Phe Asn Gln Gly Ala Thr Arg Phe				
	355		360	365
Asn His Glu Pro Pro Gly Phe Asn Gln Gly Arg Asn Phe Met Gln Gly				
	370		375	380
Ser Ser Trp Thr Asn Lys Gly Asn Gln Tyr Lys Glu Gln Arg Asn Gln				400
385		390		395
Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln				415
	405		410	
Gln Glu Lys Pro Thr Lys Ile Glu Glu Leu Leu Leu Gln Phe Ile Lys				
	420		425	430
Glu Thr Arg Ser His Gln Lys Ser Thr Asp Ala Ala Ile Arg Asn Leu				
	435		440	445
Glu Val Gln Met Gly Gln Leu Ala His Asp Lys Ala Glu Arg Pro Thr				
	450		455	460
Arg Thr Phe Gly Ala Asn Met Glu Arg Arg Thr Pro Arg Lys Asp Lys				480
465		470		475
Ala Val Leu Thr Arg Gly Gln Arg Arg Ala Gln Glu Glu Gly Lys Val				495
	485		490	
Glu Gly Glu Asp Trp Pro Glu Glu Gly Arg Thr Glu Lys Thr Glu Glu				
	500		505	510
Glu Glu Lys Val Ala Glu Glu Pro Lys Arg Thr Lys Ser Gln Arg Ala				
	515		520	525
Arg Glu Ala Lys				
530				

<210> 9

<211> 603

<212> DNA

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 9

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tcatacgga atgtctacat cttggtagct gtggattacg tctccaaatg ggtggaagcc	180
atagccacgc caaaggacga tgccagggtg gtgatcaaat ttctgaagaa gaacattttt	240
tcccgttttg gagtcccacg agccttgatt agtgataggg gaacgcactt ctgcaacaat	300
cagttgaaga aagtcttgga gcactataat gtccgacata aggtggccac accttatcac	360

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cctcagacaa atggccaagc agaaatttct aacaggggagc tcaagcgaat cctggaaaag 420
acagttgcat caacaagaaa ggattggtcc ttgaagctcg atgatgctct ctgggcctat 480
aggacagcgt tcaagactcc catcggtta tcaccatttc agctagtgtg tgggaaggca 540
tgtcatttac cagtggagct ggagtacaaa gcatattggg ctctcaagtt gctcaacttt 600
gac 603

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<210> 10
 <211> 201
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

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<400> 10
Cys Asp Lys Cys Gln Arg Thr Gly Gly Ile Ser Arg Arg Asn Glu Met
 1          5          10          15
Pro Leu Gln Asn Ile Met Glu Val Glu Ile Phe Asp Cys Trp Gly Ile
 20          25          30
Asp Phe Met Gly Pro Phe Pro Ser Tyr Gly Asn Val Tyr Ile Leu
 35          40          45
Val Ala Val Asp Tyr Val Ser Lys Trp Val Glu Ala Ile Ala Thr Pro
 50          55          60
Lys Asp Asp Ala Arg Val Val Ile Lys Phe Leu Lys Lys Asn Ile Phe
 65          70          75          80
Ser Arg Phe Gly Val Pro Arg Ala Leu Ile Ser Asp Arg Gly Thr His
 85          90          95
Phe Cys Asn Asn Gln Leu Lys Lys Val Leu Glu His Tyr Asn Val Arg
 100          105          110
His Lys Val Ala Thr Pro Tyr His Pro Gln Thr Asn Gly Gln Ala Glu
 115          120          125
Ile Ser Asn Arg Glu Leu Lys Arg Ile Leu Glu Lys Thr Val Ala Ser
 130          135          140
Thr Arg Lys Asp Trp Ser Leu Lys Leu Asp Asp Ala Leu Trp Ala Tyr
 145          150          155          160
Arg Thr Ala Phe Lys Thr Pro Ile Gly Leu Ser Pro Phe Gln Leu Val
 165          170          175
Tyr Gly Lys Ala Cys His Leu Pro Val Glu Leu Glu Tyr Lys Ala Tyr
 180          185          190
Trp Ala Leu Lys Leu Leu Asn Phe Asp
 195          200

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<210> 11
 <211> 600
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

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<400> 11
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gttcccaaga aaggtggaat gacagtggtg cgagatgaga ggaatgactt gataccaaca 120
cgaactgtca ctgggtggcg aatgtgtatc gactatcgca agctgaatga agccacacgg 180
aaggaccatt tccccttacc ttatcatggat cagatgctgg agagacttgc agggcaggca 240
tactactgtt tcttggatgg atactcggga tacaaccaga tcgcggtaga cccagagat 300
caggagaaga cggcctttac atgccccttt ggcgtctttg cttacagaag gatgccattc 360

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gggttatgta atgcaccagc cacatttcag aggtgcatgc tggccatttt ttcagacatg	420
gtggagaaaa gcatcgaggt atttatggac gacttctcgg tttttggacc ctcatttgac	480
agctgtttga ggaacctaga gaggtactt cagaggtgcg aagagactaa cttggtactg	540
aattgggaaa agtgtcattt catggttcga gagggcatag tcctaggcca caagatctca	600

<210> 12
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 12

Leu	Glu	Ala	Gly	Leu	Ile	Tyr	Pro	Ile	Ser	Asp	Ser	Ala	Trp	Val	Ser
1			5						10					15	
Pro	Val	Gln	Val	Val	Pro	Lys	Lys	Gly	Met	Thr	Val	Val	Arg	Asp	
		20						25				30			
Glu	Arg	Asn	Asp	Leu	Ile	Pro	Thr	Arg	Thr	Val	Thr	Gly	Trp	Arg	Met
		35					40				45				
Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn	Glu	Ala	Thr	Arg	Lys	Asp	His	Phe
50						55					60				
Pro	Leu	Pro	Phe	Met	Asp	Gln	Met	Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ala
65					70					75					80
Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr	Ser	Gly	Tyr	Asn	Gln	Ile	Ala	Val
			85						90					95	
Asp	Pro	Arg	Asp	Gln	Glu	Lys	Thr	Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val
			100					105					110		
Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe	Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr
		115					120					125			
Phe	Gln	Arg	Cys	Met	Leu	Ala	Ile	Phe	Ser	Asp	Met	Val	Glu	Lys	Ser
130					135						140				
Ile	Glu	Val	Phe	Met	Asp	Asp	Phe	Ser	Val	Phe	Gly	Pro	Ser	Phe	Asp
145					150					155					160
Ser	Cys	Leu	Arg	Asn	Leu	Glu	Arg	Val	Leu	Gln	Arg	Cys	Glu	Glu	Thr
			165					170					175		
Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	Cys	His	Phe	Met	Val	Arg	Glu	Gly
		180						185					190		
Ile	Val	Leu	Gly	His	Lys	Ile	Ser								
		195					200								

<210> 13
 <211> 858
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 13

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aacaaggagc gttactttgc acgtttcttg gaaatattca aaggggttaga aatcactatg	120
ccattcgggg aagccttaca gcagatgccc ctctactcca aatttatgaa agacatcctc	180
accaagaagg ggaagtatat tgacaacgag aatattgttg taggaggcaa ttgcagtgcg	240
ataatacaaa ggattctacc caagaagttt aaagaccccg gaagtgttac catcccgtgc	300
accattggga aggaagccgt aaacaaggcc ctcattgatc taggagcaag tatcaatctg	360
atgcccttgt caatgtgcaa aagaattggg aatttgaaga tagatccac caagatgacg	420

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cttcaactgg cagaccgctc aatcacaagg ccatatgggg tggtagaaga tgtcctggtc 480
aagggtacgcc acttcacttt tccggtggac tttgttatca tggatatcga agaagacact 540
gagattcccc ttattcttagg cagacccttc atgctgactg ccaactgtgt ggtggatatg 600
gggaaagggg acttagagtt gactattgat aatcagaaga tcaccttga cttatcaag 660
gcaatgaagt acccacagga gggttggaag tgcttcagaa tagaggagat tgatgaggaa 720
gatgtcagtt ttctcgagac accaaagact tcgctagaaa aagcaatggt aaatcattta 780
gactgtctaa ccagtgaaga ggaagaagat ctgaaggctt gcttggaataa cttggatcaa 840
gaagacagta ttctgag 858

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<210> 14

<211> 286

<212> PRT

<213> Artificial Sequence

<220>

<223> plant retroelement sequence

<400> 14

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Lys Glu Glu Pro Leu Ala Leu Pro Gln Asp Leu Pro Tyr Pro Met Ala
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Pro Thr Lys Lys Asn Lys Glu Arg Tyr Phe Ala Arg Phe Leu Glu Ile
20          25          30
Phe Lys Gly Leu Glu Ile Thr Met Pro Phe Gly Glu Ala Leu Gln Gln
35          40          45
Met Pro Leu Tyr Ser Lys Phe Met Lys Asp Ile Leu Thr Lys Lys Gly
50          55          60
Lys Tyr Ile Asp Asn Glu Asn Ile Val Val Gly Gly Asn Cys Ser Ala
65          70          75          80
Ile Ile Gln Arg Ile Leu Pro Lys Lys Phe Lys Asp Pro Gly Ser Val
85          90          95
Thr Ile Pro Cys Thr Ile Gly Lys Glu Ala Val Asn Lys Ala Leu Ile
100         105         110
Asp Leu Gly Ala Ser Ile Asn Leu Met Pro Leu Ser Met Cys Lys Arg
115         120         125
Ile Gly Asn Leu Lys Ile Asp Pro Thr Lys Met Thr Leu Gln Leu Ala
130         135         140
Asp Arg Ser Ile Thr Arg Pro Tyr Gly Val Val Glu Asp Val Leu Val
145         150         155         160
Lys Val Arg His Phe Thr Phe Pro Val Asp Phe Val Ile Met Asp Ile
165         170         175
Glu Glu Asp Thr Glu Ile Pro Leu Ile Leu Gly Arg Pro Phe Met Leu
180         185         190
Thr Ala Asn Cys Val Val Asp Met Gly Lys Gly Asn Leu Glu Leu Thr
195         200         205
Ile Asp Asn Gln Lys Ile Thr Phe Asp Leu Ile Lys Ala Met Lys Tyr
210         215         220
Pro Gln Glu Gly Trp Lys Cys Phe Arg Ile Glu Glu Ile Asp Glu Glu
225         230         235         240
Asp Val Ser Phe Leu Glu Thr Pro Lys Thr Ser Leu Glu Lys Ala Met
245         250         255
Val Asn His Leu Asp Cys Leu Thr Ser Glu Glu Glu Glu Asp Leu Lys
260         265         270
Ala Cys Leu Glu Asn Leu Asp Gln Glu Asp Ser Ile Pro Glu
275         280         285

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<210> 15

<211> 192

<212> DNA
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 15
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 gacaaggat ttcacgcat ctattatgct agcaagggtcc tgaatgaagc acagttgaat 120
 tatgcaacca cagaaaagga gatgctagcc attgtctttg ccttgagaa gttcagggtca 180
 tacttgatag gg 192

<210> 16
 <211> 64
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 16
 Phe Glu Leu Met Cys Asp Ala Ser Asp Tyr Ala Val Gly Ala Val Leu
 1 5 10 15
 Gly Gln Arg Lys Asp Lys Val Phe His Ala Ile Tyr Tyr Ala Ser Lys
 20 25 30
 Val Leu Asn Glu Ala Gln Leu Asn Tyr Ala Thr Thr Glu Lys Glu Met
 35 40 45
 Leu Ala Ile Val Phe Ala Leu Glu Lys Phe Arg Ser Tyr Leu Ile Gly
 50 55 60

<210> 17
 <211> 12286
 <212> DNA
 <213> Artificial Sequence

<220>
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Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser
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<210> 24

<211> 1857

<212> DNA

<213> Arabidopsis thaliana

<400> 24

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<212> DNA

<213> Pisum sativum

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<210> 26

<211> 564

<212> DNA

<213> Arabidopsis thaliana

<400> 26

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<210> 27

<211> 180

<212> DNA

<213> Arabidopsis thaliana

<400> 27

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<210> 28

<211> 192

<212> DNA

<213> Arabidopsis thaliana

<400> 28

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<210> 29

<211> 597

<212> DNA

<213> Pisum sativum

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<210> 30
 <211> 192
 <212> DNA
 <213> Pisum sativum

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<210> 31
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 <212> DNA
 <213> Pisum sativum

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<210> 32
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 <212> DNA
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1362

<210> 33

<211> 192

<212> DNA

<213> Glycine max

<400> 33

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<211> 597

<212> DNA

<213> Glycine max

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<210> 35

<211> 603

<212> DNA

<213> Glycine max

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tcatacagga atgtctacat cttggtagct gtggattacg tctccaaatg ggtggaagcc	180
atagccacgc tgaaggacga tgccagggtg gtgatcaaat ttctgaagaa gaacattttt	240
tcccatttcg gagtcccacg agccttgatt agtgatgggg gaacgcactt ctgcaacaat	300
cagttgaaga aagtccctga gcaactataat gtccgacaca aggtggccac accttatcac	360
actcagacga atggccaagc agaaatttct aacaggggagc tcaagcgaat cctggaaaag	420
acagttgcat catcaagaaa ggattgggccc ttgaagctcg atgatactct ctgggcctat	480
aggacagcgt tcaagactcc catcggttta tcaccatttc agctagtata tgggaaggca	540
tgtcatttac cagtagagct ggagcacaag gcatattggg ctctcaagtt gctcaacttt	600
gac	603

<210> 36

<211> 150

<212> DNA

<213> Glycine max

<400> 36

cctaaaatac tacaacgaca tgattgggtg tttaggataa ttgactgaaa aacctattat	60
caatttgggc ccgttgccaa ttgggtgttt gtttggtaca tttgagattt cagacttgct	120
tagatcaagt tctttttcaa ttttcttttt	150

<210> 37
 <211> 11
 <212> DNA
 <213> Glycine max

<400> 37
 tggcgccggtt g 11

<210> 38
 <211> 15
 <212> DNA
 <213> Glycine max

<400> 38
 tggcgccggtt gccgg 15

<210> 39
 <211> 27
 <212> DNA
 <213> Glycine max

<400> 39
 tttttggcgc cggtgtcggg gattttg 27

<210> 40
 <211> 9
 <212> DNA
 <213> Glycine max

<400> 40
 tttggggga 9

<210> 41
 <211> 16
 <212> DNA
 <213> Glycine max

<400> 41
 tttaatttgg gggatt 16

<210> 42
 <211> 775
 <212> DNA
 <213> Nicotiana tabacum

<400> 42
 gtgcgtaaaag aggttttttaa actggagatt atcaagtgat tggatgccgg gggttatctac 60
 cccattttacg atagttcatg aacttctccg gtgcaatgtg tcccaaagaa ggtggcatga 120
 cgggtggtcac caatgagaag aatgagttga ttcctacaag aatgggtgacc gggtggagag 180
 tgtgcatgga ctatcgcaag ctcaacaaac tcacaaggaa ggatcatttc ccatttccat 240
 tccttgacca aatgcttgat aggttggcat gtcgtgcttt ctattgcttt ctagatgtat 300
 agtcggggcta tagccaaatc tttattgctc cgtaggatca cgagaaaata cctttacatg 360
 tccctatgggt acttttgctt acaagcggat gccatttgggt ttgtgtaatg cactagcgaa 420
 ctttttatagg tgtatgatgg ctatcttcac ggacatgggtg aaggactacc tttaaagtttt 480
 catggatgac ttctcgatgg ttggggattc ctttgatgat tgcttggaaa atttggataa 540
 agtattggca agatatgaag aaacgaattt ggtactaaat tgggagaagt gtcatttcat 600

gatcgaggaa ggcattgttc ttggccacaa gatctcaaat aatggcattg aagtcgacaa 660
 ggcaaagatt aagggtgattt ctaaaacttac acctccaact ttgggtgaaag gcgtgcggag 720
 tttcttaggc cagcggggt tttaccaatt cttcataaaa gatttcacaa aggtt 775

<210> 43
 <211> 259
 <212> PRT
 <213> Nicotiana tabacum

<400> 43
 Val Arg Lys Glu Val Phe Lys Leu Glu Ile Ile Lys Glx Leu Asp Ala
 1 5 10 15
 Gly Val Ile Tyr Pro Ile Tyr Asp Ser Ser Glx Thr Ser Pro Val Gln
 20 25 30
 Cys Val Pro Lys Lys Gly Gly Met Thr Val Val Thr Asn Glu Lys Asn
 35 40 45
 Glu Leu Ile Pro Thr Arg Met Val Thr Gly Trp Arg Val Cys Met Asp
 50 55 60
 Tyr Arg Lys Leu Asn Lys Leu Thr Arg Lys Asp His Phe Pro Phe Pro
 65 70 75 80
 Phe Leu Asp Gln Met Leu Asp Arg Leu Ala Cys Arg Ala Phe Tyr Cys
 85 90 95
 Phe Leu Asp Val Glx Ser Gly Tyr Ser Gln Ile Phe Ile Ala Pro Glx
 100 105 110
 Asp His Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Tyr
 115 120 125
 Lys Arg Met Pro Phe Gly Leu Cys Asn Ala Leu Ala Asn Phe Tyr Arg
 130 135 140
 Cys Met Met Ala Ile Phe Thr Asp Met Val Lys Asp Tyr Leu Lys Val
 145 150 155 160
 Phe Met Asp Asp Phe Ser Met Val Gly Asp Ser Phe Asp Asp Cys Leu
 165 170 175
 Glu Asn Leu Asp Lys Val Leu Ala Arg Tyr Glu Glu Thr Asn Leu Val
 180 185 190
 Leu Asn Trp Glu Lys Cys His Phe Met Ile Glu Glu Gly Ile Val Leu
 195 200 205
 Gly His Lys Ile Ser Asn Asn Gly Ile Glu Val Asp Lys Ala Lys Ile
 210 215 220
 Lys Val Ile Ser Lys Leu Thr Pro Pro Thr Leu Val Lys Gly Val Arg
 225 230 235 240
 Ser Phe Leu Gly His Ala Gly Phe Tyr Gln Phe Phe Ile Lys Asp Phe
 245 250 255
 Thr Lys Val

<210> 44
 <211> 761
 <212> DNA
 <213> Nicotiana tabacum

<400> 44
 gtgcgtaaag aggtggtcaa gctgttggtat gtcgggggttg tgtaccccat ctctgatagc 60
 tcttgactt cgccggtgca atgtgtacca aagaagggttg gcatgactgt ggtgaaaaat 120
 tccaaaaatg agttgattcc gacaagaacc atcaccggtt ggagggtatg catggactac 180
 cgcaagttga ataaagtgac ctgcaaggat cacttttctt tgccatttct ggatcagatg 240
 ctagatcgac ttgctgggcg tgccttctat tgcttcttgg atgaatattc tgggtataac 300
 caaatcttga ttgctccgga agatccggaa aagaccacat tcacttgtcc gtatggcaca 360

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tttgttttct ctaggatgcc ttttaggttg tgtaatgcac cagctacatt tcagcgggtgt 420
atgatggcca ttttctccta tatggtgaaa gacatttttg aggtgttcat ggacgatttt 480
agtgttggg ggcactcatt tgatgaatgc ttgaagaatc ttgatagggt gttggcccat 540
tgtgaagaaa ccaatcttgt cctcaattgg gagaaatgcc actttatggt agaagaagga 600
atcaatctct ggcataaaat ttcaaaacat ggcattgagg tggataaaca aagatagatg 660
tgatttcaag gctccctccc cctacatccg tcaagggagt ccgatgtttt cttgggcatg 720
cggggttcta ttggagattc ataaaagact tctccaaggt t 761

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<210> 45

<211> 254

<212> PRT

<213> Nicotiana tabacum

<400> 45

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Val Arg Lys Glu Val Val Lys Leu Leu Asp Val Gly Val Val Tyr Pro
1          5          10          15
Ile Ser Asp Ser Ser Trp Thr Ser Pro Val Gln Cys Val Pro Lys Lys
20          25          30
Val Gly Met Thr Val Val Lys Asn Ser Lys Asn Glu Leu Ile Pro Thr
35          40          45
Arg Thr Ile Thr Gly Trp Arg Val Cys Met Asp Tyr Arg Lys Leu Asn
50          55          60
Lys Val Thr Cys Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met
65          70          75          80
Leu Asp Arg Leu Ala Gly Arg Ala Phe Tyr Cys Phe Leu Asp Glu Tyr
85          90          95
Ser Gly Tyr Asn Gln Ile Leu Ile Ala Pro Glu Asp Pro Glu Lys Thr
100         105         110
Thr Phe Thr Cys Pro Tyr Gly Thr Phe Val Phe Ser Arg Met Pro Phe
115         120         125
Arg Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
130         135         140
Phe Ser Tyr Met Val Lys Asp Ile Phe Glu Val Phe Met Asp Asp Phe
145         150         155         160
Ser Val Val Gly His Ser Phe Asp Glu Cys Leu Lys Asn Leu Asp Arg
165         170         175
Val Leu Ala His Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
180         185         190
Cys His Phe Met Val Glu Glu Gly Ile Asn Leu Trp His Lys Ile Ser
195         200         205
Lys His Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Ser Arg
210         215         220
Leu Pro Pro Pro Thr Ser Val Lys Gly Val Arg Cys Phe Leu Gly His
225         230         235         240
Ala Gly Phe Tyr Trp Arg Phe Ile Lys Asp Phe Ser Lys Val
245         250

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<210> 46

<211> 762

<212> DNA

<213> Nicotiana tabacum

<400> 46

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gtgcgtaagg aggtgtttta gttgttggat gttgggggttg tgtaccccat ctctgatagc 60
tcttgcatth cgccgggtgca atgtgtaccg aagaagggtg gcatgaccgt ggttgcaa 120
tcgcaaaatg ggttgattcc taccaggatc gtcaccgggt ggaaggatg catggattac 180
cgaaagtga ataaagtga cgcgaaggat cactttccat tgccttttct tgatcagatg 240

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ttagatcgac ttgctgggcg tgccttctac tgtttcttgg atgggtattc tggatacaac 300
caaattcttca ttactccgga agatcaggag aagacaacat tcacttggtcc atatggcacc 360
tttgctttttt ctaggatgcc ttttgggttg tgtaatgcac cgactacatt ctagcggtat 420
atgatggcca ttttcactga tatgggtggaa gatatttttg aggtgttcat ggacgacttt 480
agtgttgggg gtgattcatt tgatgaatgt ttgaataatc ttgatagagt gttggcccat 540
tgtaaagaaa ccaatcttgt tcttaattgg gagaaatgcc acttcatggt tgaggagggc 600
atagttcttg ggcataaaat tttaaagcat ggtatagagg tggacaaagc aaaaattgat 660
gtgatttcaa ggctccctcc ccctacttct gtcaaggagg tgagaagttt tcttaggcat 720
gcgggggttct accggagatt catcaaagat ttcaccaaag tt 762

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<210> 47

<211> 254

<212> PRT

<213> Nicotiana tabacum

<400> 47

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Val Arg Lys Glu Val Phe Lys Leu Leu Asp Val Gly Val Val Tyr Pro
1          5          10          15
Ile Ser Asp Ser Ser Cys Ile Ser Pro Val Gln Cys Val Pro Lys Lys
20          25          30
Gly Gly Met Thr Val Val Ala Asn Ser Gln Asn Gly Leu Ile Pro Thr
35          40          45
Arg Ile Val Thr Gly Trp Lys Val Cys Met Asp Tyr Arg Lys Leu Asn
50          55          60
Lys Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Leu Asp Gln Met
65          70          75          80
Leu Asp Arg Leu Ala Gly Arg Ala Phe Tyr Cys Phe Leu Asp Gly Tyr
85          90          95
Ser Gly Tyr Asn Gln Ile Phe Ile Thr Pro Glu Asp Gln Glu Lys Thr
100          105          110
Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Phe Ser Arg Met Pro Phe
115          120          125
Gly Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Tyr Met Met Ala Ile
130          135          140
Phe Thr Asp Met Val Glu Asp Ile Leu Glu Val Phe Met Asp Asp Phe
145          150          155          160
Ser Val Val Gly Asp Ser Phe Asp Glu Cys Leu Asn Asn Leu Asp Arg
165          170          175
Val Leu Ala His Cys Lys Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
180          185          190
Cys His Phe Met Val Glu Glu Gly Ile Val Leu Gly His Lys Ile Leu
195          200          205
Lys His Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Ser Arg
210          215          220
Leu Pro Pro Pro Thr Ser Val Lys Gly Val Arg Ser Phe Leu Arg His
225          230          235          240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245          250

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<210> 48

<211> 760

<212> DNA

<213> Nicotiana tabacum

<400> 48

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gcggaaggag gtcgtcaagc tggttgatgt cgggtgtgtg taccatcatat ttgatagctc 60
ttggactttg ccggtgcaat atgtgccgaa gaagggtgtg atgaccgtgg ttaccaatgt 120

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aaaaaatgag	ttgattccta	ccaggactgt	caccgggtgg	agggtgtgca	tggattacca	180
caaattgaat	aaagtgaccc	gcaaggatca	ctttccatta	ccttttcttg	atcagatgtt	240
agacagactt	gctgggtgtg	ccttctactg	tttcttggat	gggtattctg	ggtgcaacaa	300
aattttgatt	gcaccaaag	atcaggagaa	gaccaccttt	acttgtacgt	atggtacctt	360
tgtcttttct	aggatgtcat	ttgggttgtg	taatgcaccg	actacattct	agaggtgtat	420
gatggccata	tttacctaca	tggtggagga	cattttggag	gtgtttatgg	atgacttcag	480
tggtgttggt	gactagtttg	atgaatgttt	gaaaaatctt	gatagagtgt	tggcccgttg	540
tgaagaagcc	aaccttgtgc	ttaattggga	gaaatgccac	ttcatggttg	aggagggcat	600
agtccttagc	cataaaatth	caaagcatgg	tatagaggtg	gacaaagcaa	aaattgaagt	660
gatttcaagg	ctccttcccc	ctacttctgt	caagggagtt	agaagttttc	ttgggcatgc	720
ggggttctac	tggagattca	tcaaagactt	cacgaaggtt			760

<210> 49

<211> 253

<212> PRT

<213> Nicotiana tabacum

<400> 49

Arg	Lys	Glu	Val	Val	Lys	Leu	Leu	Asp	Val	Gly	Val	Val	Tyr	Pro	Ile
1				5					10					15	
Phe	Asp	Ser	Ser	Trp	Thr	Leu	Pro	Val	Gln	Tyr	Val	Pro	Lys	Lys	Gly
			20					25					30		
Gly	Met	Thr	Val	Val	Thr	Asn	Val	Lys	Asn	Glu	Leu	Ile	Pro	Thr	Arg
			35				40					45			
Thr	Val	Thr	Gly	Trp	Arg	Val	Cys	Met	Asp	Tyr	His	Lys	Leu	Asn	Lys
			50			55					60				
Val	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Leu	Asp	Gln	Met	Leu
65					70					75					80
Asp	Arg	Leu	Ala	Gly	Cys	Ala	Phe	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr	Ser
			85					90						95	
Gly	Cys	Asn	Lys	Ile	Leu	Ile	Ala	Pro	Lys	Asp	Gln	Glu	Lys	Thr	Thr
			100					105					110		
Phe	Thr	Cys	Thr	Tyr	Gly	Thr	Phe	Val	Phe	Ser	Arg	Met	Ser	Phe	Gly
			115				120					125			
Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Glx	Arg	Cys	Met	Met	Ala	Ile	Phe
			130			135					140				
Thr	Tyr	Met	Val	Glu	Asp	Ile	Leu	Glu	Val	Phe	Met	Asp	Asp	Phe	Ser
145					150					155					160
Val	Val	Gly	Asp	Glx	Phe	Asp	Glu	Cys	Leu	Lys	Asn	Leu	Asp	Arg	Val
			165					170						175	
Leu	Ala	Arg	Cys	Glu	Glu	Ala	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	Cys
			180				185						190		
His	Phe	Met	Val	Glu	Glu	Gly	Ile	Val	Leu	Ser	His	Lys	Ile	Ser	Lys
		195					200					205			
His	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Ile	Glu	Val	Ile	Ser	Arg	Leu
	210					215					220				
Leu	Pro	Pro	Thr	Ser	Val	Lys	Gly	Val	Arg	Ser	Phe	Leu	Gly	His	Ala
225					230					235					240
Gly	Phe	Tyr	Trp	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val			
			245						250						

<210> 50

<211> 762

<212> DNA

<213> Oryza sativa

<400> 50


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gtgcgtaagg aggtgtttaa gttcctgtat gccaggatta tttatctcgt accatacagc      60
gagtgggtta gcccagttca ggtcgtgccca aagaagggag gaatgacggc cgttgcaa      120
gctcaaaatg aactaatccc gcaacgaacc gtaaccggat ggagaatgtg catcgattac      180
aggaacttta acaaggctac aaaaaaggat catttccgcg tacccttcat tgatgaaatg      240
ttggaacggc tggcaaatca ttccttcttc tgtttccttg atgggtattc aggatatcat      300
caaattccca tccatccgga ggaccagagt aagactacgt tcacatgtcc atatggcacc      360
tatgcgtatc gtaggatgcc ctttggactg tgcaacactc ctgcatcttt ccaaaggtgt      420
atgatgtcta ttttctcgga catgatcgag gatatcatgg aagtcttcat ggatgacttc      480
tcgggtctatg gaaagacttt gggtcattgt ctgcagaatc tagacaaagt cttacaacga      540
tgccaagaaa aggacctagt gcttaactgg gaaaagtgcc atttcatggg ctgtgaaggg      600
atagttcttg ggcacgcagt gtccgaacga ggagtcgaag ttgatcgtgc taaaattgat      660
gtgatagatc agcttcctcc acccgtgaac atcaaaaggaa tccgcagctt ctttggtcac      720
gctggctttt atagaaggtt catcaaggac ttcacaaaag tt                          762

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<210> 51

<211> 254

<212> PRT

<213> Oryza sativa

<400> 51

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Val Arg Lys Glu Val Phe Lys Phe Leu Tyr Ala Arg Ile Ile Tyr Leu
 1          5          10          15
Val Pro Tyr Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
 20          25          30
Gly Gly Met Thr Ala Val Ala Asn Ala Gln Asn Glu Leu Ile Pro Gln
 35          40          45
Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50          55          60
Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
 65          70          75          80
Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
 85          90          95
Ser Gly Tyr His Gln Ile Pro Ile His Pro Glu Asp Gln Ser Lys Thr
 100         105         110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Arg Met Pro Phe
 115         120         125
Gly Leu Cys Asn Thr Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
 130         135         140
Phe Ser Asp Met Ile Glu Asp Ile Met Glu Val Phe Met Asp Asp Phe
 145         150         155         160
Ser Val Tyr Gly Lys Thr Leu Gly His Cys Leu Gln Asn Leu Asp Lys
 165         170         175
Val Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys
 180         185         190
Cys His Phe Met Val Cys Glu Gly Ile Val Leu Gly His Arg Val Ser
 195         200         205
Glu Arg Gly Val Glu Val Asp Arg Ala Lys Ile Asp Val Ile Asp Gln
 210         215         220
Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Phe Gly His
 225         230         235         240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245         250

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<210> 52

<211> 761

<212> DNA

<213> Oryza sativa

<400> 52
 gtgcgcaagg aggttttgaa attgctgcat gccaggatta tctatcccgt accatacagt 60
 gagagggtta gccaggtcca ggttgtgcca aagaaggag gaatggcggg cgttgcaaat 120
 gctcagaatg aactaattac gcaacaaacc gtaaccggat ggaggatgtg tatcgattac 180
 aggaaactca acaaggctac aaaaaaggat catttcccgc tacccttcat tgttgaaatg 240
 ttggaacggc tggcaaatca ttccttcttt tgtttccttg atggatatatt cggatatcat 300
 caaattccca tccatccgga ggactagagt aagactacgt tcacatgtcc atatggcacc 360
 tatgcgtatc ataggatgtc ctttggactg tgcaacgctc ctgcatcttt ccaagggtga 420
 tgatgtctat tttctcggac atgatcgagg atatcatgga agtcttcatg gatgacttct 480
 cggctctatg aaagactttc ggtcattgtc tgcaaaatct agacaaaagtc ttacaacgat 540
 gccaaagaaa ggacctgggtg cttaactggg aaaagtgaca tttcatgggc cgtgaaggga 600
 tagttcttgg gcatcgagtg ttcgaacaag gaatcgaagt tgatcatgct aaaattgatg 660
 tgatagatca gcttcctcct cccgtgaaca tcaaaggat cgcagcttc ttgggtcatg 720
 tcggctttta tagaagggtc atcaaggact tcactaaagt t 761

<210> 53
 <211> 254
 <212> PRT
 <213> Oryza sativa

<400> 53
 Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Arg Ile Ile Tyr Pro
 1 5 10 15
 Val Pro Tyr Ser Glu Arg Val Ser Pro Val Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Ala Val Val Ala Asn Ala Gln Asn Glu Leu Ile Thr Gln
 35 40 45
 Gln Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Val Glu Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Phe Gly Tyr His Gln Ile Pro Ile His Pro Glu Asp Glx Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr His Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
 130 135 140
 Phe Ser Asp Met Ile Glu Asp Ile Met Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Lys Thr Phe Gly His Cys Leu Gln Asn Leu Asp Lys
 165 170 175
 Val Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Glx His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Arg Val Phe
 195 200 205
 Glu Gln Gly Ile Glu Val Asp His Ala Lys Ile Asp Val Ile Asp Gln
 210 215 220
 Leu Pro Pro Pro Val Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 54
 <211> 762

<212> DNA

<213> Oryza sativa

<400> 54

gtgcggaag	aggtttttaa	gctcctgcat	gccgggatta	tttataccgt	tccatgcagt	60
gagtgggtca	gcacagtcca	ggttgggccg	aagatgggat	gaatgacggt	cgttgcaa	120
gctcaaaata	aacttatccc	gcaaccaacc	ataaccggat	ggaggatgtg	catagactac	180
aggaaactca	acaaggctac	aaaagaggat	cattttccgc	tacccttcat	tgatgaaatg	240
ttggaacgga	tgacaaatca	ttcctttcttc	tgtttccttg	atgggtattc	cggatatcat	300
caaattccca	tcggtccaga	ggaccagagt	aagactacgt	tcacatgtcc	atatggcacc	360
tatgcgtatc	gtaggatgtc	cttcggactg	tgcaacgctc	ctgcatcttt	ccaaagggtg	420
atgttgtcta	ttttctcggg	catgatcgaa	gatatcatga	aagtcttcat	ggatgacttc	480
tcagtttatg	gaaagacttt	cggctcattg	ctgtagaatc	tagacaaagt	cttacaacga	540
tgccaagaaa	atgacctagt	gtttaaattgg	gaaaagtgcc	attttatggg	ccgtgaaggg	600
atagttcttg	ggcatcagat	atccgaatga	ggaatcgaag	ttgatcgtgc	taaaatcgat	660
gttatagatc	ggaattcgctc	tcctgcgaat	atcaaaggaa	tccgcagctt	cttggggacat	720
gccggccttt	atagaagggt	cctcaaggac	ttcacaaaag	tt		762

<210> 55

<211> 254

<212> PRT

<213> Oryza sativa

<400> 55

Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	Ala	Gly	Ile	Ile	Tyr	Thr
1				5				10					15	
Val	Pro	Cys	Ser	Glu	Trp	Val	Ser	Thr	Val	Gln	Val	Gly	Pro	Lys
			20					25					30	Met
Gly	Glx	Met	Thr	Val	Val	Ala	Asn	Ala	Gln	Asn	Lys	Leu	Ile	Pro
		35					40					45		Gln
Pro	Thr	Ile	Thr	Gly	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu
	50					55				60				Asn
Lys	Ala	Thr	Lys	Glu	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Glu
65					70					75				Met
Leu	Glu	Arg	Met	Thr	Asn	His	Ser	Phe	Phe	Cys	Phe	Leu	Asp	Gly
				85					90					95
Ser	Gly	Tyr	His	Gln	Ile	Pro	Ile	Arg	Pro	Glu	Asp	Gln	Ser	Lys
			100					105					110	Thr
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	Arg	Arg	Met	Ser
		115					120					125		Phe
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Ser	Phe	Gln	Arg	Cys	Met	Leu	Ser
	130					135					140			Ile
Phe	Ser	Asp	Met	Ile	Glu	Asp	Ile	Met	Lys	Val	Phe	Met	Asp	Asp
145					150					155				Phe
Ser	Val	Tyr	Gly	Lys	Thr	Phe	Gly	His	Cys	Leu	Glx	Asn	Leu	Asp
				165					170					175
Val	Leu	Gln	Arg	Cys	Gln	Glu	Asn	Asp	Leu	Val	Phe	Asn	Trp	Glu
			180					185					190	Lys
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Arg	Val
		195					200					205		Ser
Glu	Glx	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Ile	Asp	Val	Ile	Asp
	210					215					220			Gln
Ile	Arg	Pro	Pro	Ala	Asn	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly
225					230					235				His
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Leu	Lys	Asp	Phe	Thr	Lys	Val	
				245					250					

<210> 56
 <211> 762
 <212> DNA
 <213> Oryza sativa

<400> 56
 gtgcgtaagg aggtcttgaa gctcttgcat gccgagatta tttatcccgt accatataga 60
 gaggtagggtta gcccgggtcta gggttatgccg aagaagggac gaatgacggg cattgcaaatt 120
 gctcaaaatg aacttattcc gcaacgaaca gtaaccggat ggaggatgtg catagattac 180
 atgaaactta acaaggctac gaaaaaggat catttcccac tacccttcat tgatgaaatg 240
 ttggaacggc tggcaaatca ttctttcttc cgtttccttg atgggtattc taggtatgat 300
 caaattccca tccatccgga ggaccaaagt aagactacgt tcacatgttc gtatgatacc 360
 tatgcttata gtaggatgtc cttcggactg tgcaacgctc ctgcatcttt ccaaagggtg 420
 atgatgtcta ttttctccga catgattaag gacattatgg aagtcttcat gcatgacttc 480
 tctatttatg gaaagacctc cggtcattgt ctacaaaatt tagacaaaat tttgcaacga 540
 tgccaagaga aggacctggg acttaattgg gaaaagtgtc atttcatggg ccgtgaaggg 600
 atagttctta gtcacgcagt gtccgaataa ggaatcgaag ttgatcgtgc taaaaactat 660
 gtaatagatt agcttccttc tcctgtgaac attaagggga tccgcaattt tttgggacat 720
 gctggccttt atagaagggt catcaaagac ttcacaaagg tt 762

<210> 57
 <211> 254
 <212> PRT
 <213> Oryza sativa

<400> 57
 Val Arg Lys Glu Val Leu Lys Leu Leu His Ala Glu Ile Ile Tyr Pro
 1 5 10 15
 Val Pro Tyr Arg Glu Trp Val Ser Pro Val Glx Val Met Pro Lys Lys
 20 25 30
 Gly Arg Met Thr Val Ile Ala Asn Ala Gln Asn Glu Leu Ile Pro Gln
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Met Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Arg Phe Leu Asp Gly Tyr
 85 90 95
 Ser Arg Tyr Asp Gln Ile Pro Ile His Pro Glu Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Ser Tyr Asp Thr Tyr Ala Tyr Arg Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Ile
 130 135 140
 Phe Ser Asp Met Ile Lys Asp Ile Met Glu Val Phe Met His Asp Phe
 145 150 155 160
 Ser Ile Tyr Gly Lys Thr Ser Gly His Cys Leu Gln Asn Leu Asp Lys
 165 170 175
 Ile Leu Gln Arg Cys Gln Glu Lys Asp Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Arg Glu Gly Ile Val Leu Ser His Arg Val Ser
 195 200 205
 Glu Glx Gly Ile Glu Val Asp Arg Ala Lys Asn Tyr Val Ile Asp Glx
 210 215 220
 Leu Pro Ser Pro Val Asn Ile Lys Gly Ile Arg Asn Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val

245

250

<210> 58
 <211> 762
 <212> DNA
 <213> Hordeum vulgare

<400> 58
 gtgcgcaagg aggttttagaa gttcctggaa gcaggtatca tctatcgtgt tgctcatagt 60
 gattggttga gtcgggtgca ttgtgtccct aagaaggag gcattaccgt tgccctaata 120
 gataaggatg aattgatccc acagaggact attactggct ataggatggt gattgatttt 180
 aggaaattga ataaagccac taggaaagat cattaccctt tgccttttat cgaccaaata 240
 cgagaaaggc tgtctaaaca cacacacttc tgctttctaa acggttatTT tggtttctcc 300
 caaataaccag ttgcacaatc tgatcaggag aaaaccactt tcacctgccc ttttggtaca 360
 tttgcttata gacgtatgac ttttggttta tgtaatgcac ctgcctcctt tcaaagatgt 420
 atgatggcta tattccctga cttttgtgaa aagattgttg aggttttcat ggatgacttc 480
 tccatttacg gatcttccct tgatgattgc ctcagcaacc ttgatcgagt cttgcagaga 540
 tgtaaagaca ccaatctttt cttgaattgg aagaagtgcc actttatggt taatgacggc 600
 atcgtcttag gacataaatt ttctgaaaga ggtattgaag tcgataaggc taaggttgat 660
 ggaatcgaga aaatgccata ccccacagat atcaaaggga taagaagttt ccttggtcat 720
 gctggtttct atagaagggt cataaaagac ttcactaagg tt 762

<210> 59
 <211> 254
 <212> PRT
 <213> Hordeum vulgare

<400> 59
 Val Arg Lys Glu Val Glx Lys Phe Leu Glu Ala Gly Ile Ile Tyr Arg
 1 5 10 15
 Val Ala His Ser Asp Trp Leu Ser Arg Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45
 Arg Thr Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Arg Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asn Gly Tyr
 85 90 95
 Phe Gly Phe Ser Gln Ile Pro Val Ala Gln Ser Asp Gln Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Thr Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Pro Asp Phe Cys Glu Lys Ile Val Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Ile Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Lys Asp Thr Asn Leu Phe Leu Asn Trp Lys Lys
 180 185 190
 Cys His Phe Met Val Asn Asp Gly Ile Val Leu Gly His Lys Phe Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Gly Ile Glu Lys
 210 215 220
 Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His

[illegible]

```
<210> 61
<211> 254
<212> PRT
<213> Hordeum vulgare
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<400>	61																
Val	Arg	Lys	Glu	Val	Leu	Lys	Phe	Leu	Glu	Ala	Gly	Ile	Ile	Tyr	Pro		
1				5					10					15			
Val	Ala	His	Asn	Asp	Trp	Val	Ser	Pro	Val	His	Cys	Val	Pro	Lys	Lys		
			20					25					30				
Gly	Cys	Ile	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Pro	His		
		35					40					45					
Arg	Ile	Ile	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Met	Asn		
	50					55					60						
Lys	Ala	Thr	Arg	Lys	Glu	His	Tyr	Pro	Leu	Pro	Phe	Ser	Asp	Gln	Met		
65					70					75					80		
Leu	Glu	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	Tyr		
				85					90					95			
Ser	Ser	Phe	Ser	Gln	Ile	Leu	Val	Ala	Gln	Ser	Asp	Gln	Glu	Lys	Thr		
			100					105					110				
Thr	Phe	Thr	Tyr	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe		
	115						120					125					
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile		
	130					135					140						
Phe	Ser	Asp	Phe	Cys	Glu	Lys	Phe	Val	Glu	Val	Phe	Met	Asp	Asp	Phe		
145				150						155					160		
Ser	Val	Tyr	Gly	Ser	Ser	Phe	Asp	Asp	Cys	Leu	Asn	Asn	Leu	Asp	Arg		
				165					170					175			
Val	Leu	Gln	Arg	Cys	Lys	Asp	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys		
			180					185					190				
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser		
	195						200				205						
Glu	Arg	Gly	Ile	Glu	Phe	Asp	Lys	Ala	Lys	Val	Gly	Ala	Ile	Lys	Lys		

210 215 220
 Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Val His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 62
 <211> 757
 <212> DNA
 <213> Hordeum vulgare

<400> 62
 gaaaagaggt tgtgaagctc ctggatgaag gtattatcta tcatgttgct catagcgatt 60
 ggggtgagtc ggtgcatagc gttcctaaga agggaggcat taccgttgct cctaatagata 120
 aggatgaatt gatcccgagc aggattatca ctggctatag gatggtgatc gatttcagga 180
 aactgaataa agccactagg aaagatcatt accctttgcc tttatcgac catatgctag 240
 aaaggttgtc caaactcaca cacttctgct ttctagacgg ttattctagt ttctcccaaa 300
 taccagttgc acaatctgat caggagaaaa ccactttcac ctgccctttc ggtacctttg 360
 cttatagacg tatgcctttt ggcttatgta atgcacctgc cacctttcaa agatgtatga 420
 tggctatatt ctctaacttt tgtgaaaata ttgtcgaggt tttcatggat gacttttccg 480
 tttacgggtc ttcttttgat gattgcctca gcaaccttga tcgagtctta cagagatgta 540
 aagacaccaa tcttgtcttg aatggggaga agtgccactt tatggttaat gaaggcatcg 600
 tcttaggaca taaaatttct gaaagaggta ttgaagtcga taaggctaag gttgatgcaa 660
 tcgacaaaat gccatacccc acagatatca aaggataaag aagtttcctt ggtcatgggtg 720
 gtttctatag aaggtttatc aaagatttca caaaggt 757

<210> 63
 <211> 251
 <212> PRT
 <213> Hordeum vulgare

<400> 63
 Lys Glu Val Val Lys Leu Leu Asp Glu Gly Ile Ile Tyr His Val Ala
 1 5 10 15
 His Ser Asp Trp Val Ser Pro Val His Ser Val Pro Lys Lys Gly Gly
 20 25 30
 Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln Arg Ile
 35 40 45
 Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn Lys Ala
 50 55 60
 Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Ile Asp His Met Leu Glu
 65 70 75 80
 Arg Leu Ser Lys Leu Thr His Phe Cys Phe Leu Asp Gly Tyr Ser Ser
 85 90 95
 Phe Ser Gln Ile Pro Val Ala Gln Ser Asp Gln Glu Lys Thr Thr Phe
 100 105 110
 Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu
 115 120 125
 Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile Phe Ser
 130 135 140
 Asn Phe Cys Glu Asn Ile Val Glu Val Phe Met Asp Asp Phe Ser Val
 145 150 155 160
 Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg Val Leu
 165 170 175
 Gln Arg Cys Lys Asp Thr Asn Leu Val Leu Asn Gly Glu Lys Cys His
 180 185 190
 Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser Glu Arg

Gly	Ile	195					200				205				
	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Ile	Asp	Lys	Met	Pro	
	210				215					220					
Tyr	Pro	Thr	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His	Gly	Gly
225					230					235					240
Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys					
				245					250						

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<210> 64
<211> 740
<212> DNA
<213> Hordeum vulgare
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[illegible]

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<210> 65
<211> 247
<212> PRT
<213> Hordeum vulgare
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<400> 65																
Val	Arg	Lys	Glu	Val	Ile	Lys	Phe	Leu	Glu	Glu	Gly	Ile	Ile	Tyr	Pro	
1				5					10					15		
Val	Ala	His	Ser	Asp	Trp	Val	Ser	Pro	Val	His	Cys	Ile	Pro	Lys	Lys	
			20					25					30			
Gly	Gly	Ile	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Pro	Glx	
		35					40					45				
Arg	Ile	Ile	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Leu	Asn	
	50					55					60					
Lys	Ala	Thr	Arg	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met	
65					70					75				80		
Leu	Glu	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Leu	Phe	Leu	Asp	Gly	Tyr	
				85					90					95		
Thr	Gly	Phe	Ser	Gln	Ile	Pro	Val	Ala	Gln	Phe	Asp	Gln	Glu	Lys	Thr	
			100					105					110			
Thr	Leu	Thr	Glx	His	Phe	Gly	Thr	Phe	Ala	Tyr	Ile	Arg	Met	Pro	Phe	
		115					120					125				
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile	
	130					135					140					
Phe	Ser	Asp	Phe	Cys	Glu	Lys	Ile	Val	Asn	Val	Phe	Met	Asp	Asn	Phe	
145					150					155					160	
Ser	Val	Tyr	Gly	Cys	Ser	Phe	Asp	Asp	Cys	Leu	Asn	Asn	Val	Asp	Arg	
				165					170					175		
Val	Leu	Gln	Arg	Cys	Lys	Asp	Thr	Asn	Val	Val	Leu	Asn	Trp	Glu	Lys	

180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Glu Arg Gly Ile Lys Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220
 Met Pro Tyr Pro Thr Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe
 245

<210> 66
 <211> 762
 <212> DNA
 <213> Avena sativa

<400> 66
 gtgcgaaagg aggttttcaa gctcatggat gctggtatta tttaccctat tgctgatagt 60
 gaatgggtta gtcattgttca ttgtgttcct aaaaagggag gtattaccgt tgtccctaata 120
 gataatgatg agcttattcc tcaaagaata gtggtaggct ataggatgtg catcgatttt 180
 aggaaagtca ataaagttac taagaaagat cactaccgcg ttccttttat tgatcaaagt 240
 ttggaaagat tttctaaaaa gaccattttt tgttttcttg atggttattc tggtttctct 300
 caaattgttg ttaaacaaca agatcaagaa aaaactactt ttacttgccc ttatggaact 360
 tatgcttata gatgtatgcc ttttggttta tgtaatgctc cttctacttt cctaagggtgc 420
 atgtctgcta tctttcatgg tttttgtgag gaaattgtag aagtgttcat ggacgacttt 480
 tctgtctacg gaacttcttt tgataattgt ctgcacaacc ttgataaagt tttacagaga 540
 tgtgaaggaa ctaattcttg tcttaattgg gagaaatgcc acttcatggt taatgaaggg 600
 attgttcttg ggcataaagt ttctaaaaga ggcataagaag ttgatagagc taagggttgag 660
 gcaattgaga agatgccatg tccaagagac atcaaaggta ttcgtagtat ccttggtcat 720
 gctggtttct ataggagggt catcaaagac ttcacaaagg tt 762

<210> 67
 <211> 254
 <212> PRT
 <213> Avena sativa

<400> 67
 Val Arg Lys Glu Val Phe Lys Leu Met Asp Ala Gly Ile Ile Tyr Pro
 1 5 10 15
 Ile Ala Asp Ser Glu Trp Val Ser His Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Pro Asn Asp Asn Asp Glu Leu Ile Pro Gln
 35 40 45
 Arg Ile Val Val Gly Tyr Arg Met Cys Ile Asp Phe Arg Lys Val Asn
 50 55 60
 Lys Val Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Phe Ser Lys Lys Thr His Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Phe Ser Gln Ile Val Val Lys Gln Gln Asp Gln Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Tyr Arg Cys Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ser Thr Phe Leu Arg Cys Met Ser Ala Ile
 130 135 140
 Phe His Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys

				165					170					175		
Val	Leu	Gln	Arg	Cys	Glu	Gly	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	
			180					185					190			
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser	
		195					200					205				
Lys	Arg	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Val	Glu	Ala	Ile	Glu	Lys	
	210					215					220					
Met	Pro	Cys	Pro	Arg	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Ile	Leu	Gly	His	
225					230					235					240	
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val			
				245					250							

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<210> 68
<211> 762 . .
<212> DNA
<213> Avena sativa
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[illegible]

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<210> 69 . . . .  
<211> 254  
<212> PRT  
<213> Avena sativa
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<400> 69															
Val	Arg	Lys	Glu	Val	Phe	Lys	Phe	Leu	Asp	Ala	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Ile	Ala	Asp	Ser	Gln	Trp	Val	Ser	Leu	Val	His	Cys	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Ile	Thr	Val	Val	Pro	Asn	Glu	Asp	Asn	Glu	Leu	Ile	Pro	Gln
		35					40					45			
Arg	Val	Val	Val	Val	Tyr	Arg	Met	Cys	Ile	Asp	Phe	Arg	Arg	Ile	Asn
	50					55					60				
Lys	Val	Thr	Arg	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met
65					70					75				80	
Leu	Glu	Arg	Leu	Ser	Lys	Lys	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	His
				85					90					95	
Ser	Gly	Phe	Ser	Gln	Ile	Val	Val	Lys	Ala	Gln	Asp	Gln	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Asp	Tyr	Arg	Arg	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Ser	Ala	Ile
	130					135					140				
Phe	His	Gly	Phe	Cys	Glu	Glu	Ile	Val	Glu	Val	Phe	Met	Asp	Asp	Phe

145 150 155 160
 Ser Val Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys
 165 170 175
 Phe Leu Gln Arg Phe Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Arg Ala Lys Ile Glu Ala Ile Glu Asn
 210 215 220
 Met Pro Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Ser Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 70

<211> 756

<212> DNA

<213> Avena sativa

<400> 70

aaggagggttt ttaaactcct tgatgttggt attatttacc ctattgctga tagtgaatgg 60
 gtagtcttg ttcattgtgt tcctaaaaag ggaggtatta ccgttggtcc taatgataat 120
 gatgagctta ttcctcaaag aatagtggta ggctatagga tgtgcataga ttttaggaaa 180
 gtaataaaag ttactaagaa agatcactac ccgcttcctt ttattgatca aatgttggaa 240
 aggttgtcta aaaagacca tttttgtttt cttgatgggt actctagctt ctctcaaatt 300
 gctgttaaag aacaagatca agaaaaaact acttttactt gcccttatgg aacttttgct 360
 tatagacgta tgctattgg tttatgtaat gctcctgcta cttttcaaag gtgtatgtct 420
 gctatatttc atgggttttg tgaggaaatt gtagaagtgt tcatggatga cttttctgtc 480
 tatggaactt cttttgataa ttgcctgcac aaccttgata aagttttgca gagatgtgaa 540
 gaaactaata ttgttcttaa ttggggagaaa ttccacttca tggttaatga agggattgtc 600
 cttgggcata aagtttctaa aagaggcata gaagttgata gagctaaggt tgaggcaatt 660
 gagaagatgc catgcccaag agacatcaaa ggtatacgta gtatccttgg tcatgctggg 720
 ttctatagaa ggtttatcaa agacttcaca aaggtt 756

<210> 71

<211> 252

<212> PRT

<213> Avena sativa

<400> 71

Lys Glu Val Phe Lys Leu Leu Asp Val Gly Ile Ile Tyr Pro Ile Ala
 1 5 10 15
 Asp Ser Glu Trp Val Ser Leu Val His Cys Val Pro Lys Lys Gly Gly
 20 25 30
 Ile Thr Val Val Pro Asn Asp Asn Asp Glu Leu Ile Pro Gln Arg Ile
 35 40 45
 Val Val Gly Tyr Arg Met Cys Ile Asp Phe Arg Lys Val Asn Lys Val
 50 55 60
 Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met Leu Glu
 65 70 75 80
 Arg Leu Ser Lys Lys Thr His Phe Cys Phe Leu Asp Gly Tyr Ser Ser
 85 90 95
 Phe Ser Gln Ile Ala Val Lys Gln Gln Asp Gln Glu Lys Thr Thr Phe
 100 105 110
 Thr Cys Pro Tyr Gly Thr Phe Ala Tyr Arg Arg Met Pro Ile Gly Leu
 115 120 125
 Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Ser Ala Ile Phe His

130	135	140
Gly Phe Cys Glu Glu Ile Val Glu Val Phe Met Asp Asp Phe Ser Val		
145	150	155
Tyr Gly Thr Ser Phe Asp Asn Cys Leu His Asn Leu Asp Lys Val Leu		
	165	170
Gln Arg Cys Glu Glu Thr Asn Ile Val Leu Asn Trp Glu Lys Phe His		
	180	185
Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser Lys Arg		
	195	200
Gly Ile Glu Val Asp Arg Ala Lys Val Glu Ala Ile Glu Lys Met Pro		
	210	215
Cys Pro Arg Asp Ile Lys Gly Ile Arg Ser Ile Leu Gly His Ala Gly		
225	230	235
Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val		
	245	250

<210> 72
 <211> 748
 <212> DNA
 <213> Secale cereale

<400> 72	
gtgcggaag aggtcttta actcctagag gcaggtatta actatcccat tgctgatagc	60
cagcgggtaa gtcattgtcca ttgtgttcct aagaaaggag gtatgactgt cgtccctaag	120
gataaagatg aatttatccc gcaaagaata gttacagggt ataggatggg aattgatttt	180
cgtaagttaa ataaagctac tatgaaagat cattaccctc tgccatttat tgatcaaagc	240
ccagacaggt tatccaaaca tactcatttc tgctttctag atggttattc tggtttctct	300
caaatacctt tgtcaaaggg ggatcaagaa aagaccacct ttacttgctc tttcgggtacc	360
tttgcttata gaggtatgcc ttttggttta tgtaattgcac ctgctacctt tcaaagatgt	420
atgatcggtt tattctctgt cttttttgaa aagattggtg aggtattcat ggatgatttc	480
tccgtttatg gaacttcttt tgatgattgc ttaagcaacc ttgatcgagt tttgcagaga	540
tgtgaagata ctaaccttgt cttgaattgg gagaagtgcc actttatggt taatgaaggc	600
attttcttgg gacataaaat ttctgaaaga ggtactgaag ttgagaaagc taaagtggat	660
gctattgaaa agatgccatg ccctaaggat atgaaaggta tacgaagttt ccttggtcac	720
gctgggtttt ataggagggt cataaaa	748

<210> 73
 <211> 249
 <212> PRT
 <213> Secale cereale

<400> 73	
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Asn Tyr Pro	
1	5
Ile Ala Asp Ser Gln Arg Val Ser His Val His Cys Val Pro Lys Lys	
	10
	15
	20
Gly Gly Met Thr Val Val Pro Lys Asp Lys Asp Glu Phe Ile Pro Gln	
	25
	30
	35
Arg Ile Val Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn	
	40
	45
	50
Lys Ala Thr Met Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met	
	55
	60
	65
Pro Asp Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr	
	70
	75
	80
	85
	90
	95
Ser Gly Phe Ser Gln Ile Pro Leu Ser Lys Gly Asp Gln Glu Lys Thr	
	100
	105
	110
Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Gly Met Pro Phe	

[illegible]

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<210> 74
<211> 762
<212> DNA
<213> Secale cereale
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[illegible]

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<210> 75
<211> 254
<212> PRT
<213> Secale cereale
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<400> 75															
Val	Arg	Lys	Glu	Val	Val	Lys	Leu	Pro	Glu	Ala	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Val	Ala	Asp	Ser	Gln	Trp	Val	Ser	His	Val	His	Cys	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Met	Thr	Val	Val	Pro	Asn	Asp	Lys	His	Glu	Leu	Ile	Pro	Gln
		35					40					45			
Arg	Ile	Val	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Leu	Asn
	50					55					60				
Lys	Ala	Thr	Lys	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met
65					70					75				80	
Leu	Asp	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	Tyr
				85					90					95	
Tyr	Gly	Phe	Ser	Gln	Ile	Pro	Val	Ser	Lys	Gly	Asp	Gln	Glu	Lys	Thr

			100					105				110			
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile
	130					135					140				
Leu	Ser	Asp	Phe	Glx	Glu	Lys	Ile	Val	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Ser	Val	Tyr	Gly	Thr	Ser	Phe	Asp	Asp	Tyr	Leu	Ser	Asn	Asn	Asp	Arg
				165				170						175	
Val	Leu	Gln	Arg	Cys	Glu	Asp	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
		180						185				190			
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	Gln	Lys	Ile	Ser
		195					200					205			
Glu	Arg	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Val	Glu	Lys
	210					215					220				
Met	Pro	Cys	Pro	Lys	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230					235					240
Val	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

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<210> 76
<211> 762
<212> DNA
<213> Secale cereale
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<400>	76									
gtgcgtaagg	aggtggttaa	gctcctagaa	gcaggtatta	tctatccagt	tgctgatagt					60
cagtgggtaa	gtcatgtcca	ttatgttcct	aagaaaaggag	gtatgactgt	tgtcccataat					120
gataaagatg	aattgatccc	gcaaagaata	gttacagggt	ataggatggg	aagtgatttc					180
cgtaagttga	ataaagccac	taagaaagat	cattaccctt	tgccatttat	tgatcaaatg					240
ctagaaaggt	tatccaaaca	tactcatttc	ttctttctag	atggttattc	tggtttctct					300
caaataacctg	tgtcaaaaagg	ggatcaagaa	aagaccacct	ttacttgtac	ttcoggtacc					360
tttgcttata	gacgtatgcc	ttttggttta	tgtaatgcac	ctgctacctt	tcaaagatgc					420
atgatggcta	tattctctga	cttttgtgaa	aagattgttg	aggtattcat	ggatgatttc					480
tccgtttacg	gaacttcttt	tगतatttgc	ttaagcaacc	ttgatcgagt	tttgcacaga					540
tgtgaagaca	ctaacccttg	cttgaattgc	gagaagtgcc	actttatggg	taatgaaggc					600
attgtcttgg	gacataaaat	ttctgaaata	ggatttgaag	ttgacaaaagc	taaagttgat					660
gctattgaaa	agatgccatg	cgcaaaggac	atcaaaggta	tacggagttt	ccttggtcat					720
gccgggtttt	ataggaggtt	catcaaagat	ttctcaaagg	tt						762

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<210> 77
<211> 254
<212> PRT
<213> Secale cereale
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<400> 77															
Val	Arg	Lys	Glu	Val	Val	Lys	Leu	Leu	Glu	Ala	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Val	Ala	Asp	Ser	Gln	Trp	Val	Ser	His	Val	His	Tyr	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Met	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Pro	Gln
		35					40					45			
Arg	Ile	Val	Thr	Gly	Tyr	Arg	Met	Val	Ser	Asp	Phe	Arg	Lys	Leu	Asn
	50					55					60				
Lys	Ala	Thr	Lys	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met
65					70					75					80
Leu	Glu	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Phe	Phe	Leu	Asp	Gly	Tyr

				85						90					95				
Ser	Gly	Phe	Ser	Gln	Ile	Pro	Val	Ser	Lys	Gly	Asp	Gln	Glu	Lys	Thr				
			100					105					110						
Thr	Phe	Thr	Cys	Thr	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe				
		115					120					125							
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile				
		130				135					140								
Phe	Ser	Asp	Phe	Cys	Glu	Lys	Ile	Val	Glu	Val	Phe	Met	Asp	Asp	Phe				
145				150					155					160					
Ser	Val	Tyr	Gly	Thr	Ser	Phe	Asp	Asp	Cys	Leu	Ser	Asn	Leu	Asp	Arg				
			165				170						175						
Val	Leu	Gln	Arg	Cys	Glu	Asp	Thr	Asn	Leu	Val	Leu	Asn	Cys	Glu	Lys				
		180					185						190						
Cys	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser				
		195				200					205								
Glu	Ile	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Ile	Glu	Lys				
	210					215				220									
Met	Pro	Cys	Ala	Lys	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His				
225				230					235					240					
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Ser	Lys	Val						
			245				250												

<210> 78

<211> 759

<212> DNA

<213> Secale cereale

<400> 78

gtgcgcaagg	aagtttttaa	gtttctagag	gcaggtataa	tctatccagt	tgctgatagc	60
cagtgggttaa	gtcctgtcca	ttgtgtccct	aagaagggag	gtatgactgt	agttccta	120
gataaagatg	aattgatctc	gcaaagaatt	gttacaggtt	ataggatggt	aattgatttt	180
cgcaaattaa	ataaagccac	taagaaagat	caataccctt	tgctttttat	tgatcaaatg	240
ctagaaagggt	tatccaaaca	caccattttt	tgctttctag	atgggttatc	tagtttctct	300
caaataccta	tgtcaaaagg	ggataaagaa	aagaccactt	ttacttgtcc	ctttgggtact	360
ttgcttatag	acgtatgcct	tttggtttat	gtaatgcac	tgctaccttt	caaacatgca	420
tgatggctat	actctatgat	ttttgtgaaa	gaatgttgat	gttttcatgg	atgatttttg	480
tatttacgaa	acttcttttg	atgattgctt	gagcaacctt	gatcgagttt	tgacagagatg	540
tgaagaaact	aatcttgtct	tgaactggga	aaagtccac	tttatgggta	atgaaggcat	600
tgcttgggac	ataaaatttc	tgaaagaggt	accgaagttg	acaaagctaa	agttgatgct	660
gttgaaaaga	tgccatgtcc	caaggacatc	aaaggtataa	gaagtttcct	tggtcatgcc	720
gggttttata	ggaggtttat	caaggacttc	accaaggtt			759

<210> 79

<211> 254

<212> PRT

<213> Secale cereale

<400> 79

Val	Arg	Lys	Glu	Val	Phe	Lys	Phe	Leu	Glu	Ala	Gly	Ile	Ile	Tyr	Pro
1				5				10						15	
Val	Ala	Asp	Ser	Gln	Trp	Val	Ser	Pro	Val	His	Cys	Val	Pro	Lys	Lys
			20				25					30			
Gly	Gly	Met	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Ser	Gln
		35				40					45				
Arg	Ile	Val	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Leu	Asn
	50					55				60					
Lys	Ala	Thr	Lys	Lys	Asp	Gln	Tyr	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met

65					70					75					80
Leu	Glu	Arg	Leu	Ser	Lys	His	Thr	His	Phe	Cys	Phe	Leu	Asp	Gly	Tyr
				85					90					95	
Ser	Ser	Phe	Ser	Gln	Ile	Pro	Met	Ser	Lys	Gly	Asp	Lys	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Ser	Ala	Thr	Phe	Gln	Thr	Cys	Met	Met	Ala	Ile
	130					135					140				
Leu	Tyr	Asp	Phe	Cys	Glu	Arg	Ile	Val	Asp	Val	Phe	Met	Asp	Asp	Phe
145					150				155					160	
Cys	Ile	Tyr	Glu	Thr	Ser	Phe	Asp	Asp	Cys	Leu	Ser	Asn	Leu	Asp	Arg
				165					170					175	
Val	Leu	Gln	Arg	Cys	Glu	Glu	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
			180					185					190		
Ser	His	Phe	Met	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser
		195					200					205			
Glu	Arg	Gly	Thr	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ala	Val	Glu	Lys
	210					215					220				
Met	Pro	Cys	Pro	Lys	Asp	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
225				230					235						240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

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<210> 80
<211> 761
<212> DNA
<213> Triticum aestivum
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<400>	80						
gtgcgtaagg	aggttctcaa	gtttctggag	gtaggtataa	tttatcccgt	tgctgatagt		60
cagtgggtaa	gtcctgtcca	ttgtgtccct	aagaagggag	gtattactgt	tgtcccta	aat	120
gataaagatg	aattgattcc	tcaaagaatt	attacggtta	taggatggta	attgatttcc		180
gcaaattaa	taaagccact	aagagagatc	attaccacct	acctttttatt	gatcaaattc		240
tagaaaagatt	atgcaaacat	acacattatt	gcttccaaga	tggttatcct	ggtttttctc		300
aaataacctgt	gtcggctaaa	gatcaatcaa	agactacttt	tacatgccct	tttggtactt		360
ttgcttatag	atgtatgcct	tttggtttat	gtaatgcacc	tgctaccttt	caaagatgca		420
tgatggctat	attctctgat	ttttgtgaaa	agatttgtga	ggttttcatg	gatgactttt		480
ccgtctatgg	ttcctctttt	gatgattgct	tgagcaatct	tgatcgagtt	ttgcagagat		540
gtgaagaaac	taactctgtc	ttgaattggg	aaaagtgtca	ctttatgggt	aatgaaggta		600
ttgtcttggg	gcacaaagtt	tctgaaagag	gtattgaagt	tgataaagcc	aagggttgaca		660
ctattgaaaa	gataccatgt	cccaaggaca	tcaaaggtac	aagaagtttc	cttggtcacg		720
ccqgattttaa	taggaggttc	ataaaaagatt	tcacaaaggt	t			761

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<210> 81
<211> 254
<212> PRT
<213> Triticum aestivum
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<400> 81															
Val	Arg	Lys	Glu	Val	Leu	Lys	Phe	Leu	Glu	Val	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Val	Ala	Asp	Ser	Gln	Trp	Val	Ser	Pro	Val	His	Cys	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Ile	Thr	Val	Val	Pro	Asn	Asp	Lys	Asp	Glu	Leu	Ile	Pro	Gln
		35					40					45			
Arg	Ile	Ile	Thr	Gly	Tyr	Arg	Met	Val	Ile	Asp	Phe	Arg	Lys	Leu	Asn

50			55			60									
Lys 65	Ala	Thr	Lys	Arg	Asp 70	His	Tyr	Pro	Leu	Pro 75	Phe	Ile	Asp	Gln	Ile 80
Leu	Glu	Arg	Leu	Cys 85	Lys	His	Thr	His	Tyr 90	Cys	Phe	Gln	Asp	Gly 95	Tyr
Pro	Gly	Phe	Ser 100	Gln	Ile	Pro	Val	Ser 105	Ala	Lys	Asp	Gln	Ser 110	Lys	Thr
Thr	Phe	Thr 115	Cys	Pro	Phe	Gly	Thr 120	Phe	Ala	Tyr	Arg	Cys 125	Met	Pro	Phe
Gly	Leu 130	Cys	Asn	Ala	Pro	Ala 135	Thr	Phe	Gln	Arg	Cys 140	Met	Met	Ala	Ile
Phe 145	Ser	Asp	Phe	Cys	Glu 150	Lys	Ile	Cys	Glu 155	Val	Phe	Met	Asp	Asp	Phe 160
Ser	Val	Tyr	Gly 165	Ser	Ser	Phe	Asp	Asp 170	Cys	Leu	Ser	Asn	Leu 175	Asp	Arg
Val	Leu	Gln 180	Arg	Cys	Glu	Glu	Thr 185	Asn	Leu	Val	Leu	Asn 190	Trp	Glu	Lys
Cys	His 195	Phe	Met	Val	Asn	Glu 200	Gly	Ile	Val	Leu	Gly 205	His	Lys	Val	Ser
Glu 210	Arg	Gly	Ile	Glu	Val 215	Asp	Lys	Ala	Lys	Val 220	Asp	Thr	Ile	Glu	Lys
Ile 225	Pro	Cys	Pro	Lys 230	Asp	Ile	Lys	Gly	Thr 235	Arg	Ser	Phe	Leu	Gly 240	His
Ala	Gly	Phe 245	Tyr	Arg	Arg	Phe	Ile	Lys 250	Asp	Phe	Thr	Lys	Val		

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<210> 82
<211> 780
<212> DNA
<213> Triticum aestivum
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<400>	82						
gtgcggaagg	aggtgtttaa	gtcctttag	gcaggtataa	tttatcccg	tgctgatagt		60
aagtgggtaa	ttcctgtcca	ttaagtgatc	gtgattactg	ttgttcctaa	gaagggaggt		120
attaccgttg	ttcctaata	ttaaagatga	ttgattccctc	aaagaacccat	tactgggtat		180
aggatggtaa	ttgatttccg	caaattaaat	aaggctacta	aaaaatatca	ttacccctta		240
ccttttatcg	atcaaagtct	agaaagatta	tccaaacata	cacatttttg	ctttctagat		300
ggttactctg	gtttctctca	aatacctgtg	tcagccaaag	atcaatcaa	gactactttt		360
acatgccctt	ttggtacttt	tgcttataga	cgtatgcctt	ttggtttatg	taatgcacct		420
gctacctttc	aaagatacat	gatggctata	ttatctgact	tttgtgaaaa	gatttgtag		480
gttttcatgg	acgactcttc	catctatgga	tcttcttttg	atgattgctt	gagcaacctt		540
gatcgagttt	tgcaagatg	tgaagaaact	tatcttgtct	tgaattggga	aaagtgccaa		600
tttatggtta	atgaaggat	tgctcctggg	cataaagttt	ctgaaagagg	tattcgagtt		660
gataaagcca	aggttgatgc	tattgaaaag	atgccatgtc	ccatggacat	caaaggtata		720
agaagtttcc	ttggtcatgc	cggtttttat	aggaggttca	taaaagactt	cacgaaggtt		780

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<210> 83
<211> 260
<212> PRT
<213> Triticum aestivum
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<400> 83															
Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	Glu	Ala	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Val	Ala	Asp	Ser	Lys	Trp	Val	Ile	Pro	Val	His	Glx	Val	Ile	Val	Ile
			20					25					30		
Thr	Val	Val	Pro	Lys	Lys	Gly	Gly	Ile	Thr	Val	Val	Pro	Asn	Asp	Lys

35	40	45
Asp Glu Leu Ile Pro Gln Arg Thr Ile Thr Gly Tyr Arg Met Val Ile		
50	55	60
Asp Phe Arg Lys Leu Asn Lys Ala Thr Lys Lys Tyr His Tyr Pro Leu		
65	70	75
Pro Phe Ile Asp Gln Met Leu Glu Arg Leu Ser Lys His Thr His Phe		
85	90	95
Cys Phe Leu Asp Gly Tyr Ser Gly Phe Ser Gln Ile Pro Val Ser Ala		
100	105	110
Lys Asp Gln Ser Lys Thr Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala		
115	120	125
Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln		
130	135	140
Arg Tyr Met Met Ala Ile Leu Ser Asp Phe Cys Glu Lys Ile Cys Glu		
145	150	155
Val Phe Met Asp Asp Ser Ser Ile Tyr Gly Ser Ser Phe Asp Asp Cys		
165	170	175
Leu Ser Asn Leu Asp Arg Val Leu Gln Arg Cys Glu Glu Thr Tyr Leu		
180	185	190
Val Leu Asn Trp Glu Lys Cys Gln Phe Met Val Asn Glu Gly Ile Val		
195	200	205
Leu Gly His Lys Val Ser Glu Arg Gly Ile Arg Val Asp Lys Ala Lys		
210	215	220
Val Asp Ala Ile Glu Lys Met Pro Cys Pro Met Asp Ile Lys Gly Ile		
225	230	235
Arg Ser Phe Leu Gly His Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp		
245	250	255
Phe Thr Lys Val		
260		

<210> 84
 <211> 762
 <212> DNA
 <213> Triticum aestivum

<400> 84

gtgcgtaagg	aggtattcaa	gcttctggag	gcagggtataa	tttatcccg	tgttgatagt	60
caatgggtaa	gtcctgtcca	ttgtgtcctt	aagaaggag	gtattactgt	tgtcccta	120
gataaagatg	aattgattcc	gcaaagaatt	atcacagggt	ataggatggt	aattgatttc	180
cgtaagttaa	ataaagctac	taagaaagat	cattaccctt	tacctttat	tgatcaa	240
ttagaaagat	tatgcaaaca	tacacattat	tgctttctag	atgggtattc	tgggttctct	300
caaatacctg	tgtagctaa	ggatcaatca	aagactactt	ttacatgccc	ttttggtact	360
tttggttata	gacgtatgcc	tttcgattta	tgtaatgcac	ctgctacctt	tcaa	420
atgatggcta	tattctctga	cttttgcgaa	aagattttgtg	agggtttcat	ggacgacttt	480
tccgtctatg	gttcctctta	tgatgattgc	ttgagcaatc	ttaatcgagt	tttgagaga	540
tgtgaagaaa	ctaattctgt	cttgaattgg	gaaaagtgcc	actttatggt	taatgaagg	600
attgtcttgg	ggcacaaagt	ttctgaacga	ggtattgaag	ttgataaggc	caagggtgat	660
gctattgaaa	agatgacatg	tcccaaggac	atcaaaggta	taagaagttt	ccttggtcac	720
gccagatttt	ataggaggtt	cataaaagac	ttcacaaagg	tt		762

<210> 85
 <211> 254
 <212> PRT
 <213> Triticum aestivum

<400> 85
 Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro

1	5	10	15
Val Val Asp	Ser Gln Trp Val Ser	Pro Val His Cys Val	Leu Lys Lys
	20	25	30
Gly Gly Ile	Thr Val Val Pro Asn Asp	Lys Asp Glu Leu Ile	Pro Gln
	35	40	45
Arg Ile Ile	Thr Gly Tyr Arg Met Val	Ile Asp Phe Arg Lys	Leu Asn
	50	55	60
Lys Ala Thr	Lys Lys Asp His Tyr Pro	Leu Pro Phe Ile Asp	Gln Met
65	70	75	80
Leu Glu Arg	Leu Cys Lys His Thr His	Tyr Cys Phe Leu Asp	Gly Tyr
	85	90	95
Ser Gly Phe	Ser Gln Ile Pro Val Ser	Ala Lys Asp Gln Ser	Lys Thr
	100	105	110
Thr Phe Thr	Cys Pro Phe Gly Thr Phe	Gly Tyr Arg Arg Met	Pro Phe
	115	120	125
Asp Leu Cys	Asn Ala Pro Ala Thr Phe	Gln Ile Cys Met Met	Ala Ile
	130	135	140
Phe Ser Asp	Phe Cys Glu Lys Ile Cys	Glu Val Phe Met Asp	Asp Phe
145	150	155	160
Ser Val Tyr	Gly Ser Ser Tyr Asp Asp	Cys Leu Ser Asn Leu	Asn Arg
	165	170	175
Val Leu Gln	Arg Cys Glu Glu Thr Asn	Leu Val Leu Asn Trp	Glu Lys
	180	185	190
Cys His Phe	Met Val Asn Glu Gly Ile Val	Leu Gly His Lys Val	Ser
	195	200	205
Glu Arg Gly	Ile Glu Val Asp Lys Ala	Lys Val Asp Ala Ile	Glu Lys
	210	215	220
Met Thr Cys	Pro Lys Asp Ile Lys Gly	Ile Arg Ser Phe Leu	Gly His
225	230	235	240
Ala Arg Phe	Tyr Arg Arg Phe Ile Lys	Asp Phe Thr Lys Val	
	245	250	

<210> 86

<211> 762

<212> DNA

<213> Triticum aestivum

<400> 86

gtgcggaaag	aggtgctcaa	gcttctggag	gcaggtataa	tttatcccgt	tgctgagagt	60
cagtgggtaa	gtcctgtcca	ttgtgtccct	aagaagggag	gtattactgt	tgccctaata	120
gataaagatg	aattgattcc	tcaaagaatt	attacagggt	ataggatggg	aattgatttc	180
cgcaaattaa	ataaagccac	caagaaagat	cattaccctt	taccttttat	tgatcaaatg	240
ctagaaagat	tatgcaaaca	tacacattat	tgcttcctag	atggttatct	tggtttctct	300
caaatacctg	tgtcggctaa	agatcaatca	aagactactt	ttacatgccc	ttttggtact	360
tttgcttata	gacgtatgcc	ttttggttta	tgtaatgcac	cttctacctt	tcaaagatgc	420
atgatggcta	tattctctga	tttttgtgaa	aagatttgtg	aggttttcat	ggacgaattt	480
tccgtctatg	gttcctcttt	tgatgattgc	ttgagcaatc	ctgatcgagt	tttgcagaga	540
tgtgaagaaa	ctaattctgt	cttgaattgg	gaaaagtgcc	actttatggt	taatgaaggt	600
attgtcttgg	ggcacaaaag	ttctgaaaga	ggtattgaa	ttgataaagc	caaggttgac	660
gctattgaaa	agatgccatg	tcccaaggac	atcaaaggta	taagaagttt	ccttggtcac	720
gccggatttt	ataggagggt	cataaaagac	ttcacaaagg	tt		762

<210> 87

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 87

Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Gly Ile Ile Tyr Pro
 1 5 10 15
 Val Ala Glu Ser Gln Trp Val Ser Pro Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Pro Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45
 Arg Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe Arg Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Cys Lys His Thr His Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Phe Ser Gln Ile Pro Val Ser Ala Lys Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ser Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Ser Asp Phe Cys Glu Lys Ile Cys Glu Val Phe Met Asp Glu Phe
 145 150 155 160
 Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Pro Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220
 Met Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 88

<211> 762

<212> DNA

<213> Triticum aestivum

<400> 88

gtgcgtaagg aggttttcaa gttccttgag gcagggtatta cttatcccgt tgctgatagt 60
 gaatgggtaa gccctctcca ttgtgttcoct aaaaagggag gtattaccgt tggtcttaat 120
 gataaagatg aattgatccc gcaaataatt attacagggt ataggatggg aattgatttc 180
 cataagttaa ataaagctac taagaaagat cattaccctt tacctcttat tgatcaaatt 240
 ctagaaagac tatccaaaca cacacatttc tgctttctag atgggtatatac tggtttctct 300
 caaataacctg tgtcagtga ggatcaatct aaaactactt ttacttgccc ttttggtact 360
 tttgcttata gacttatgcc ttttggttta tgtaatgcac ctacttcctt tcaaagatgc 420
 atgatggcta tattctctgt tttttgtgaa aatatttgtg aggtattcat ggatgatttc 480
 tccgtttatg gatcctcttt tgatgattgt ttgagcaacc ttgatcgagt tttgcagaga 540
 tgcgaagaca ctagtctcat cctgaattgg gaaaagtgtc actttatggg taatgaaggc 600
 attgtcttgg ggcataagat ttccgagaga ggtattgaag ttgacaaagc caaagttgat 660
 gctattgaaa agattccatg tcccaaggac ataaaaggta taagaagttt ccttggtcat 720
 gctgggtttt ataggagggt catcaaagac ttctcaaagg tt 762

<210> 89

<211> 254

<212> PRT

<213> Triticum aestivum

<400> 89

Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Ile Thr Tyr Pro
 1 5 10 15
 Val Ala Asp Ser Glu Trp Val Ser Pro Leu His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Val Leu Asn Asp Lys Asp Glu Leu Ile Pro Gln
 35 40 45
 Ile Ile Ile Thr Gly Tyr Arg Met Val Ile Asp Phe His Lys Leu Asn
 50 55 60
 Lys Ala Thr Lys Lys Asp His Tyr Pro Leu Pro Leu Ile Asp Gln Ile
 65 70 75 80
 Leu Glu Arg Leu Ser Lys His Thr His Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Thr Gly Phe Ser Gln Ile Pro Val Ser Val Lys Asp Gln Ser Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Leu Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Thr Ser Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Ser Val Phe Cys Glu Asn Ile Cys Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Tyr Gly Ser Ser Phe Asp Asp Cys Leu Ser Asn Leu Asp Arg
 165 170 175
 Val Leu Gln Arg Cys Glu Asp Thr Ser Leu Ile Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Asn Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Val Asp Ala Ile Glu Lys
 210 215 220
 Ile Pro Cys Pro Lys Asp Ile Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val
 245 250

<210> 90

<211> 791

<212> DNA

<213> Gossypium hirsutum

<400> 90

gtgcgcaagg aggtttttaa gctacttgat gacgggatga tctatcccat atctaacagt 60
 aattgggtta gccaggtaca catagtacca aaaaagacca gtgcaaccgt aatcgagaat 120
 tcggcagggtg agatagttcc cactcgggtc caaaacgggt ggagagtatg catcgattac 180
 aggaagtga attccttaac tcggaaggat cactttccac ttctttttat tgaccagatg 240
 ttagaacgtt tagctggaaa gtctcattat ttagaacgtt tagctggaaa gtctcattat 300
 tgttggttgg atggttacta aggttttttc cagatcccag tggcaccgga ggatcaagaa 360
 agacaatgtt tacgtgcca tttggcacgt tttcttacag acggatgcog ttcggactct 420
 gtaatgcacc agccagtttt cataggtgca tggtaagtat attttcagac tacgtcgata 480
 aaattatcga ggtgttcacg gacgacttta ctgtatatgg tgagtccttc gaggttaagtc 540
 tgacgaacct tgcaaaaatt ttggaaaagat gcttagaatt taatcttggt ctaaattatg 600
 agaaaatgcca ttttatggta gacaagggat tagttctagg tcatattatt tctgctgatg 660
 gaatttctgt tgataaagca aaaatcaaca tcattaactc actaccatac cccacaactg 720
 tgaggagat ttggtctttc cttggtcatg caggtttcta caagtgggtc atcaaagact 780
 tttcaaaagt t 791

<210> 91
 <211> 264
 <212> PRT
 <213> Gossypium hirsutum

<400> 91
 Val Arg Lys Glu Val Leu Lys Leu Leu Asp Asp Gly Met Ile Tyr Pro
 1 5 10 15
 Ile Ser Asn Ser Asn Trp Val Ser Pro Val His Ile Val Pro Lys Lys
 20 25 30
 Thr Ser Ala Thr Val Ile Glu Asn Ser Ala Gly Glu Ile Val Pro Thr
 35 40 45
 Arg Val Gln Asn Gly Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Ser Leu Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly Lys Ser His Tyr Leu Glu Arg Leu Ala Gly
 85 90 95
 Lys Ser His Tyr Cys Cys Leu Asp Gly Tyr Glx Gly Phe Phe Gln Ile
 100 105 110
 Pro Val Ala Pro Glu Asp Gln Glu Lys Thr Met Phe Thr Cys Pro Phe
 115 120 125
 Gly Thr Phe Ser Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro
 130 135 140
 Ala Ser Phe His Arg Cys Met Val Ser Ile Phe Ser Asp Tyr Val Asp
 145 150 155 160
 Lys Ile Ile Glu Val Phe Met Asp Asp Phe Thr Val Tyr Gly Glu Ser
 165 170 175
 Phe Glu Val Ser Leu Thr Asn Leu Ala Lys Ile Leu Glu Arg Cys Leu
 180 185 190
 Glu Phe Asn Leu Val Leu Asn Tyr Glu Lys Cys His Phe Met Val Asp
 195 200 205
 Lys Gly Leu Val Leu Gly His Ile Ile Ser Ala Asp Gly Ile Ser Val
 210 215 220
 Asp Lys Ala Lys Ile Asn Ile Ile Asn Ser Leu Pro Tyr Pro Thr Thr
 225 230 235 240
 Val Arg Glu Ile Trp Ser Phe Leu Gly His Ala Gly Phe Tyr Lys Trp
 245 250 255
 Phe Ile Lys Asp Phe Ser Lys Val
 260

<210> 92
 <211> 763
 <212> DNA
 <213> Gossypium hirsutum

<400> 92
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 aattgggtta gtccagtcca catagtaccc aaaaagaccg gtgtaaccgt aattgagaat 120
 tcagcaggtg agatggttcc cacttaagtc cgaaacggtc ggagagtatg catcgattac 180
 aggaagttga attccttaac tcggaaagat cactttccac ttctttttat tgatcagatg 240
 ttagaacatt tagccagaaa gtctcattat tgttgctcgg atgggttactc aggttttttc 300
 cagatcccaa tggcactaaa ggatcaagaa aagatgacat ttacgtgccc atttggcattg 360
 ttcgcttata gaaggatgct gtttcagact ttgcaatgca ccaaccatgt ttcagagggtg 420
 catgataagt atattttttg actatgttaa gaaaataatt gaggtgttca tggacgaatt 480
 tactgtatat agtgagtcct tcgaggtata tttgtcaaat ctagaaaaat ttttggaag 540
 atgccttagaa ttttaacttg ttctaaatta tgagaattgc tatttaattg tagacaaggg 600

attagttcta ggtcatatca tttctgctaa gggaatttct gtcgataaag taaaaattaa 660
 catcataagc tcaataccat accccacaac tgtgaggag attcgttctt tccttagtca 720
 tataggtttc tataggcgat tcatcaagga cttttcaaaa gtt 763

<210> 93

<211> 254

<212> PRT

<213> Gossypium hirsutum

<400> 93

Val	Arg	Lys	Glu	Val	Val	Lys	Leu	Leu	Asp	Ser	Gly	Met	Ile	Tyr	Pro
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Ile	Ser	Asp	Asn	Asn	Trp	Val	Ser	Pro	Val	His	Ile	Val	Pro	Lys	Lys
		20						25					30		
Thr	Gly	Val	Thr	Val	Ile	Glu	Asn	Ser	Ala	Gly	Glu	Met	Val	Pro	Thr
	35						40					45			
Glx	Val	Arg	Asn	Gly	Arg	Arg	Val	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55					60				
Ser	Leu	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Leu	Phe	Ile	Asp	Gln	Met
65					70					75					80
Leu	Glu	His	Leu	Ala	Arg	Lys	Ser	His	Tyr	Cys	Cys	Leu	Asp	Gly	Tyr
			85						90					95	
Ser	Gly	Phe	Phe	Gln	Ile	Pro	Met	Ala	Leu	Lys	Asp	Gln	Glu	Lys	Met
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Met	Phe	Ala	Tyr	Arg	Arg	Met	Ser	Phe
		115					120					125			
Arg	Leu	Cys	Asn	Ala	Pro	Thr	Met	Phe	Gln	Arg	Cys	Met	Ile	Ser	Ile
	130					135					140				
Phe	Phe	Asp	Tyr	Val	Lys	Lys	Ile	Ile	Glu	Val	Phe	Met	Asp	Glu	Phe
145					150					155					160
Thr	Val	Tyr	Ser	Glu	Ser	Phe	Glu	Val	Tyr	Leu	Ser	Asn	Leu	Glu	Lys
			165						170					175	
Phe	Leu	Glu	Arg	Cys	Leu	Glu	Phe	Asn	Leu	Val	Leu	Asn	Tyr	Glu	Asn
		180						185					190		
Cys	Tyr	Leu	Met	Val	Asp	Lys	Gly	Leu	Val	Leu	Gly	His	Ile	Ile	Ser
	195						200					205			
Ala	Lys	Gly	Ile	Ser	Val	Asp	Lys	Val	Lys	Ile	Asn	Ile	Ile	Ser	Ser
	210					215					220				
Ile	Pro	Tyr	Pro	Thr	Thr	Val	Arg	Glu	Ile	Arg	Ser	Phe	Leu	Ser	His
225					230					235					240
Ile	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Ser	Lys	Val		
				245					250						

<210> 94

<211> 723

<212> DNA

<213> Gossypium hirsutum

<400> 94

gtgcgtaagg	aggttttgaa	attgttgat	gctggaatga	tatactcgat	ctttgacagt	60
gattgggtta	gctgggttca	tgtcgtgcc	aagaaaactg	gcgtgacagt	ggtgaaaaac	120
tcatcaggag	agctagtccc	taccgcagtc	cagaatcgat	ggagggtttg	catcgattac	180
aggaagtga	acgcagctac	ccgaaatgac	cattttccac	ttcccttcat	tgatcaaatg	240
ctcgagcgat	tagctaataa	gacccattat	tgttgtctcg	atgggtactc	aggacttttc	300
caaattccgg	tggcacctga	ggatcaagac	aaaacaactt	tcacgtgccc	ctttggaacg	360
tttgcgata	gaagaatgtc	gtttggactc	tgtaatgtc	cggccacttt	ccagagatgt	420
atggtgagca	tattctctga	ttatgtcgag	aaaatcattg	aattcttcat	ggatgacttc	480

acgggtgtacg gtaactcttt taacgaatgt ctcgataatc ttgctaagat attacagaga 540
 tgccatagaat ttaactcttg tttaaattat gaaaaatgcc acttcatggg tgacaaagga 600
 ttaattttgg gtcatatagt ttcttcagaa ggtattgagg tcaataaagc aaaaacgaat 660
 attattgact cattacctta ccccagattt tacagacgat tcataaagga cttcacaaaa 720
 gtt 723

<210> 95

<211> 241

<212> PRT

<213> *Gossypium hirsutum*

<400> 95

Val Arg Lys Glu Val Leu Lys Leu Leu Asp Ala Gly Met Ile Tyr Ser
 1 5 10 15
 Ile Phe Asp Ser Asp Trp Val Ser Trp Val His Val Val Pro Lys Lys
 20 25 30
 Thr Gly Val Thr Val Val Lys Asn Ser Ser Gly Glu Leu Val Pro Thr
 35 40 45
 Arg Val Gln Asn Arg Trp Arg Val Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Ala Ala Thr Arg Asn Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn Lys Thr His Tyr Cys Cys Leu Asp Gly Tyr
 85 90 95
 Ser Gly Leu Phe Gln Ile Pro Val Ala Pro Glu Asp Gln Asp Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Thr Phe Ala Tyr Arg Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Val Ser Ile
 130 135 140
 Phe Ser Asp Tyr Val Glu Lys Ile Ile Glu Phe Phe Met Asp Asp Phe
 145 150 155 160
 Thr Val Tyr Gly Asn Ser Phe Asn Glu Cys Leu Asp Asn Leu Ala Lys
 165 170 175
 Ile Leu Gln Arg Cys Leu Glu Phe Asn Leu Val Leu Asn Tyr Glu Lys
 180 185 190
 Cys His Phe Met Val Asp Lys Gly Leu Ile Leu Gly His Ile Val Ser
 195 200 205
 Ser Glu Gly Ile Glu Val Asn Lys Ala Lys Thr Asn Ile Ile Asp Ser
 210 215 220
 Leu Pro Tyr Pro Arg Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys
 225 230 235 240
 Val

<210> 96

<211> 762

<212> DNA

<213> *Lycopersicon esculentum*

<400> 96

gtgcggaaag aggttgtgaa gctgttagat acgggtattg tctagccaat ttcggacaac 60
 aagtaggtta gtccagtaca atgtgaacct aaaaaggagg acataacggg gatcactaat 120
 gaaaaaatg agttgatccc aaccatgata gtcacataat ggagaatatg catggattac 180
 aggaaattga atgaagccac caggaaggac cattaccggg tcccttttat tgatcagatg 240
 ttggaccggg tggctgggga ataattattat tgttttctta atggctattt acggtacaac 300
 caaattgtga tttcacaaa ggattaagag aaaaccactt tcacttgccc gtatggtaca 360

tatgctttca	aaaagatacc	ttttgggtta	tgaaatgcct	cggtactttt	ccaatgatgc	420
atgatggcta	tttttcatga	tatggttgaa	gattttgttg	agatattcat	gaatgatttc	480
tcagtgtttg	gggattcttt	tgatatgtgc	ttggagaatt	tggacagtgt	gttggctagt	540
tgtgaagaaa	ctaattcttt	cctaaactgg	gaataatagc	aatttctagt	aaaggaaggg	600
attatgctag	gacataaggt	gtcaaagaga	ggtatggaag	ttgatagtgc	caaagtggag	660
gttattgaaa	agcttcccc	tcctatatct	gttaaaggga	tgcaaagttt	tctgggtcat	720
gttgggttct	ataggagatt	cataaaagac	ttcacaaagg	tt		762

<210> 97

<211> 254

<212> PRT

<213> *Lycopersicon esculentum*

<400> 97

Val	Arg	Lys	Glu	Val	Val	Lys	Leu	Leu	Asp	Thr	Gly	Ile	Val	Glx	Pro
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Ile	Ser	Asp	Asn	Lys	Glx	Val	Ser	Pro	Val	Gln	Cys	Glu	Pro	Lys	Lys
			20					25					30		
Gly	Asp	Ile	Thr	Val	Ile	Thr	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Thr
			35				40					45			
Met	Ile	Val	Thr	Glx	Trp	Arg	Ile	Cys	Met	Asp	Tyr	Arg	Lys	Leu	Asn
			50				55				60				
Glu	Ala	Thr	Arg	Lys	Asp	His	Tyr	Pro	Val	Pro	Phe	Ile	Asp	Gln	Met
65					70					75				80	
Leu	Asp	Arg	Leu	Ala	Gly	Glu	Glx	Tyr	Tyr	Cys	Phe	Leu	Asn	Gly	Tyr
				85					90					95	
Leu	Arg	Tyr	Asn	Gln	Ile	Val	Ile	Ser	Pro	Lys	Asp	Glx	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Phe	Lys	Lys	Ile	Pro	Phe
		115				120						125			
Gly	Leu	Glx	Asn	Ala	Ser	Ala	Thr	Phe	Gln	Glx	Cys	Met	Met	Ala	Ile
		130				135					140				
Phe	His	Asp	Met	Val	Glu	Asp	Phe	Val	Glu	Ile	Phe	Met	Asn	Asp	Phe
145					150					155				160	
Ser	Val	Phe	Gly	Asp	Ser	Phe	Asp	Met	Cys	Leu	Glu	Asn	Leu	Asp	Ser
			165						170					175	
Val	Leu	Ala	Ser	Cys	Glu	Glu	Thr	Asn	Leu	Phe	Leu	Asn	Trp	Glu	Glx
			180					185					190		
Glx	Gln	Phe	Leu	Val	Lys	Glu	Gly	Ile	Met	Leu	Gly	His	Lys	Val	Ser
		195					200					205			
Lys	Arg	Gly	Met	Glu	Val	Asp	Ser	Ala	Lys	Val	Glu	Val	Ile	Glu	Lys
		210				215					220				
Leu	Pro	Pro	Pro	Ile	Ser	Val	Lys	Gly	Met	Gln	Ser	Phe	Leu	Gly	His
225					230					235				240	
Val	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 98

<211> 689

<212> DNA

<213> *Lycopersicon esculentum*

<400> 98

cgaaaggagg	tggatgaaact	ggaaattatc	aagtagttgg	atgctagagt	aatctatcca	60
atcgccgata	gtagttgggt	atgcctagtt	cagtgtgtac	caaagaaagg	gggaatgact	120
gtgggtcccca	acgaaaagaa	tgaacttggt	cgaatgagac	cggttactgg	atggagggtg	180
tgcattggatt	accgtaaact	gaactcatag	actgaaaaag	actattttca	tatgcccttc	240

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atggatcaga tgttgatag acttgccgga aaagggtggt attgttttct tgatgggtat 300
tcgggggtata atcagatttc tattgcacca gaagatcaag agaaaaccac tttcacttgt 360
ccatacggga cttttgcatt cagaagaatg tcgtttgggt tgtgcaatgc acccgcaacc 420
tttcagagat ggatgatgtc aatattttct gacatgatgg aggatactat agagggtttt 480
atggatgatt tttctgtggt tgggtattca ttcgagcggg gcttgtccaa tttatctgag 540
gttcttaaga gatgtgaaga ctgcaatttg gtactaaact gggaaaagtg tcatttcatg 600
gtgaaagagg gtattgtgtt gggcatcgc atttcagaaa agggcatgca tgtttttact 660
ggtgattcat caaagacttc acaaagggt 689

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<210> 99

<211> 229

<212> PRT

<213> Lycopersicon esculentum

<400> 99

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Arg Lys Glu Val Val Lys Leu Glu Ile Ile Lys Glx Leu Asp Ala Arg
1 5 10 15
Val Ile Tyr Pro Ile Ala Asp Ser Ser Trp Val Cys Leu Val Gln Cys
20 25 30
Val Pro Lys Lys Gly Gly Met Thr Val Val Pro Asn Glu Lys Asn Glu
35 40 45
Leu Val Arg Met Arg Pro Val Thr Gly Trp Arg Val Cys Met Asp Tyr
50 55 60
Arg Lys Leu Asn Ser Glx Thr Glu Lys Asp Tyr Phe His Met Pro Phe
65 70 75 80
Met Asp Gln Met Leu Asp Arg Leu Ala Gly Lys Gly Trp Tyr Cys Phe
85 90 95
Leu Asp Gly Tyr Ser Gly Tyr Asn Gln Ile Ser Ile Ala Pro Glu Asp
100 105 110
Gln Glu Lys Thr Thr Phe Thr Cys Pro Tyr Gly Thr Phe Ala Phe Arg
115 120 125
Arg Met Ser Phe Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Trp
130 135 140
Met Met Ser Ile Phe Ser Asp Met Met Glu Asp Thr Ile Glu Val Phe
145 150 155 160
Met Asp Asp Phe Ser Val Val Gly Asp Ser Phe Glu Arg Cys Leu Ser
165 170 175
Asn Leu Ser Glu Val Leu Lys Arg Cys Glu Asp Cys Asn Leu Val Leu
180 185 190
Asn Trp Glu Lys Cys His Phe Met Val Lys Glu Gly Ile Val Leu Gly
195 200 205
His Arg Ile Ser Glu Lys Gly Met His Val Phe Thr Gly Asp Ser Ser
210 215 220
Lys Thr Ser Gln Arg
225

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<210> 100

<211> 760

<212> DNA

<213> Lycopersicon esculentum

<400> 100

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agtgggttag tctagtacaa tgtgtaccta aaaaggagg catggcaatg attactaatg 120
aaaacaatga gtttatccca accagcacag tcacaagatg gcgaatatgc atgaattaca 180
cgaagttaat gaagccacta ggaagaatca ttacccaatt ctttttattg attatatgtt 240
ggaccggtta gctgggcaag aatattattg ttttttggt tactaatcag ggtacaacta 300

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aatttttgatt gcaccagagg atcaagagaa aacaactttc acttgcccgt atggtacata 360
tgcttttcaag aggatacctt ttgggttatg caatgctctg tctaatttcc aaagatgcat 420
gatgactatt tttcatgata tggttgaata ttttgaggat atattcatgg atgatttctt 480
agtgttttgg gagtcttttg atagatgctt ggagaatttg aacaggttgt tagctagggtg 540
cgaacaaact aatcttgtcc tgaactggga aaaatgtcat tttttagtaa aggaaggga 600
tttttcgggg cataaggtgt aaaagatagg gctggaagtt gatcatgaca aagtgggaagt 660
aattgaaaag atctcctctc ccatttttgt gaaacgggtg agaagtttac taggtcatgc 720
tgagttttac aggatattca tcaaggactt ctcaaaggtt 760

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<210> 101
 <211> 254
 <212> PRT
 <213> *Lycopersicon esculentum*

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<400> 101
Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Pro
1 5 10 15
Ile Ser Asp Asn Lys Trp Val Ser Leu Val Gln Cys Val Pro Lys Lys
20 25 30
Gly Gly Met Ala Met Ile Thr Asn Glu Asn Asn Glu Phe Ile Pro Thr
35 40 45
Ser Thr Val Thr Arg Trp Arg Ile Cys Met Asn Tyr Thr Lys Leu Asn
50 55 60
Glu Ala Thr Arg Lys Asn His Tyr Pro Ile Leu Phe Ile Asp Tyr Met
65 70 75 80
Leu Asp Arg Leu Ala Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Tyr Glx
85 90 95
Ser Gly Tyr Asn Glx Ile Leu Ile Ala Pro Glu Asp Gln Glu Lys Thr
100 105 110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Arg Ile Pro Phe
115 120 125
Gly Leu Cys Asn Ala Leu Ser Asn Phe Gln Arg Cys Met Met Thr Ile
130 135 140
Phe His Asp Met Val Glu Tyr Phe Glu Asp Ile Phe Met Asp Asp Phe
145 150 155 160
Leu Val Phe Trp Glu Ser Phe Asp Arg Cys Leu Glu Asn Leu Asn Arg
165 170 175
Leu Leu Ala Arg Cys Glu Gln Thr Asn Leu Val Leu Asn Trp Glu Lys
180 185 190
Cys His Phe Leu Val Lys Glu Gly Asn Phe Ser Gly His Lys Val Glx
195 200 205
Lys Ile Gly Leu Glu Val Asp His Asp Lys Val Glu Val Ile Glu Lys
210 215 220
Ile Ser Ser Pro Ile Phe Val Lys Arg Val Arg Ser Leu Leu Gly His
225 230 235 240
Ala Glu Phe Tyr Arg Ile Phe Ile Lys Asp Phe Ser Lys Val
245 250

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<210> 102
 <211> 776
 <212> DNA
 <213> *Lycopersicon esculentum*

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<400> 102
gtgcggaaag aagtgtttta actggaatca ttaaattggtt ggatgctgga gtaatatatc 60
cgatctccga tagtagttgg gtatgcccta ttcagtgtgt acctaaagaaa ggggggaatga 120
ctgtggtccc caataagaaa aatgaacttg ttctaagtag accggttact ggaggggtggg 180

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tgtgtatgga	ttaccgtaaa	ttaaattgcat	ggactgaaaa	agaccattttt	cctatgccct	240
tcatggatca	gatgttgga	agacttgccg	aaaaagggtg	gtactgtttt	cttgatggat	300
agtcagggtg	taattagatt	tctattgcac	cagaagatca	agagaaaacc	acattttactt	360
gtccatatgg	gacctttgca	ttgaagagaa	tgtcgtttgg	gttgtgcaat	gcacccgcca	420
cattttcacag	atgtaaaaaat	gttgatattc	ttcgacatgg	tggatgatac	tattgatgct	480
tttatggatg	atttttctct	tgttggtgaa	tcattcgaga	ggtgtttgaa	ccatttatct	540
gatgtcctta	agagatgtga	agactgcaat	ttagtactaa	attgggaaaa	atgccacttc	600
atggtgaaaa	aaggtattgt	tttgggtcat	cgcattccag	aaaagggtcat	agaggttgat	660
cgagctaaag	tagaggtaat	agagagactt	ccccactat	ctctgtaaaa	ggtgtgagaa	720
gctttcttgg	gcatgcaagt	ttttaccgga	gattcatcaa	agacttcaca	aaagtt	776

<210> 103

<211> 258

<212> PRT

<213> *Lycopersicon esculentum*

<400> 103

Ala	Glu	Arg	Ser	Val	Glx	Thr	Gly	Ile	Ile	Lys	Trp	Leu	Asp	Ala	Gly
1				5					10					15	
Val	Ile	Tyr	Pro	Ile	Ser	Asp	Ser	Ser	Trp	Val	Cys	Pro	Ile	Gln	Cys
			20					25					30		
Val	Pro	Lys	Lys	Gly	Gly	Met	Thr	Val	Val	Pro	Asn	Lys	Lys	Asn	Glu
		35					40					45			
Leu	Val	Leu	Met	Arg	Pro	Val	Thr	Gly	Gly	Trp	Val	Cys	Met	Asp	Tyr
	50					55					60				
Arg	Lys	Leu	Asn	Ala	Trp	Thr	Glu	Lys	Asp	His	Phe	Pro	Met	Pro	Phe
65					70				75					80	
Met	Asp	Gln	Met	Leu	Asp	Arg	Leu	Ala	Glu	Lys	Gly	Trp	Tyr	Cys	Phe
			85						90					95	
Leu	Asp	Gly	Glx	Ser	Gly	Tyr	Asn	Glx	Ile	Ser	Ile	Ala	Pro	Glu	Asp
		100						105					110		
Gln	Glu	Lys	Thr	Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Phe	Ala	Leu	Lys
	115						120					125			
Arg	Met	Ser	Phe	Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	His	Arg	Cys
	130					135					140				
Lys	Met	Leu	Ile	Phe	Phe	Asp	Met	Val	Asp	Asp	Thr	Ile	Asp	Ala	Phe
145					150					155				160	
Met	Asp	Asp	Phe	Ser	Leu	Val	Gly	Glu	Ser	Phe	Glu	Arg	Cys	Leu	Asn
			165					170					175		
His	Leu	Ser	Asp	Val	Leu	Lys	Arg	Cys	Glu	Asp	Cys	Asn	Leu	Val	Leu
		180						185					190		
Asn	Trp	Glu	Lys	Cys	His	Phe	Met	Val	Lys	Lys	Gly	Ile	Val	Leu	Gly
	195						200					205			
His	Arg	Ile	Pro	Glu	Lys	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Val	Glu
	210					215					220				
Val	Ile	Glu	Arg	Leu	Pro	Pro	Pro	Ile	Ser	Val	Lys	Gly	Val	Arg	Ser
225					230					235				240	
Phe	Leu	Gly	His	Ala	Ser	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr
			245					250						255	
Lys	Val														

<210> 104

<211> 761

<212> DNA

<213> *Solanum tuberosum*

<400> 104
 gtgcggaagg aggtacttaa attggtggat gcacggattg tgtacccaat atcagacagt 60
 aaatgggtaa gtccagtaaa gtgtgtgccc aagaagggca gaatgacggt gttgactaat 120
 gagaagaatg aggtaatccc cacaagaaca gtgactgggt gacggatttg catggactac 180
 atgaagttga acgacgccac cagaaaggac cattatccgg tacctttcat tgataaaata 240
 ttggataggt tggcaggaca tgagtactat tgttttcttg gtgtctactc aggggtacaat 300
 cagattgtta ttgcaataga ggactaggtg aaaaccacct tcacctgttc gtatggcaca 360
 tatgcgttca agcacatgcc attcggcttg tgcaatgccc tggccacatt tcagagatgc 420
 atgttggcaa tcttccatga tatggtggag gattttgttg aagttttcat ggatgacttc 480
 ttggtgtttg gtgagtcctt tgaactttgt ttgactaatt ttgacagatt tcttgctagg 540
 tgtgaagaga cgaatctggt gataaactga tagaagtgtc actttctggt tcgagaggga 600
 attgtgttgg gacacaagat ctccaaaaat gggctgaaag ttgacaaagc caacgtagag 660
 gttattgaga aattgccacc cccatcacag tgaaggtaat taaaagctta ctaggacatg 720
 cttggtttta tacgaggttc atcaaagact tcacaaaggt t 761

<210> 105

<211> 254

<212> PRT

<213> Solanum tuberosum

<400> 105

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	Asp	Ala	Arg	Ile	Val	Tyr	Pro
1				5					10					15	
Ile	Ser	Asp	Ser	Lys	Trp	Val	Ser	Pro	Val	Lys	Cys	Val	Pro	Lys	Lys
			20					25					30		
Gly	Arg	Met	Thr	Val	Leu	Thr	Asn	Glu	Lys	Asn	Glu	Val	Ile	Pro	Thr
			35				40					45			
Arg	Thr	Val	Thr	Gly	Glx	Arg	Ile	Cys	Met	Asp	Tyr	Met	Lys	Leu	Asn
	50					55					60				
Asp	Ala	Thr	Arg	Lys	Asp	His	Tyr	Pro	Val	Pro	Phe	Ile	Asp	Lys	Ile
65					70					75					80
Leu	Asp	Arg	Leu	Ala	Gly	His	Glu	Tyr	Tyr	Cys	Phe	Leu	Gly	Val	Tyr
				85					90					95	
Ser	Gly	Tyr	Asn	Gln	Ile	Val	Ile	Ala	Ile	Glu	Asp	Glx	Val	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Ser	Tyr	Gly	Thr	Tyr	Ala	Phe	Lys	His	Met	Pro	Phe
			115				120					125			
Gly	Leu	Cys	Asn	Ala	Leu	Ala	Thr	Phe	Gln	Arg	Cys	Met	Leu	Ala	Ile
	130					135					140				
Phe	His	Asp	Met	Val	Glu	Asp	Phe	Val	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Leu	Val	Phe	Gly	Glu	Ser	Phe	Glu	Leu	Cys	Leu	Thr	Asn	Phe	Asp	Arg
				165					170					175	
Phe	Leu	Ala	Arg	Cys	Glu	Glu	Thr	Asn	Leu	Val	Ile	Asn	Glx	Glx	Lys
			180					185					190		
Cys	His	Phe	Leu	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser
	195						200					205			
Lys	Asn	Gly	Leu	Lys	Val	Asp	Lys	Ala	Asn	Val	Glu	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Ile	Thr	Val	Lys	Val	Ile	Lys	Ser	Leu	Leu	Gly	His
225					230					235					240
Ala	Trp	Phe	Tyr	Thr	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 106

<211> 760

<212> DNA

<213> Solanum tuberosum

<400> 106

gtgcgtaaag	agggttttcaa	actgctagat	gtcgggtattg	tatatccgat	ttcagaaagc	60
aaatgggtca	gcccagttta	gtgtgtgcct	aaaaaaagag	gcatgccggt	gatcaccaat	120
gaaaaaaatg	agttgattcc	aaccaggaca	gtgacagggt	ggcgaatatg	catggattat	180
aggaaattga	atgaggccac	cagaaaggat	cactgcccgg	ttccttttat	tgatcagatg	240
ctggacaggt	tagttgggca	agaatattat	tgtttcctgg	aaggctattc	aggatacaac	300
caaattgtga	ttgcaccaga	ggaccaggag	aaaactacat	tcacttgtct	gtatgggaca	360
tatgctttca	agtgactgcc	gtttgggcta	tgcaatgctc	cagccacctt	ccaaagatga	420
atgatggcta	tctttcatga	tatggttgaa	gattttgtgg	agatattcat	ggatgacttc	480
tcagtcttta	gggagtcctt	tgataggtgt	ttggagaatt	gggacagggt	gctggctaga	540
tgcgaggaaa	ctaattctcat	cctaaactgg	aaaaaatgtc	atttcctagt	aaatgaaggg	600
attgtattgg	gccataaggt	gtcaaagaga	gggctggaag	ttgatcgtgc	caaagtggaa	660
gttattgaaa	aactacctcc	tccaatctgt	taaaggggtg	agaagctttc	tgggtcatgc	720
tggtttttac	aggagattta	taaaggactt	cacaaaggtt			760

<210> 107

<211> 254

<212> PRT

<213> Solanum tuberosum

<400> 107

Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	Asp	Val	Gly	Ile	Val	Tyr	Pro
1				5					10					15	
Ile	Ser	Glu	Ser	Lys	Trp	Val	Ser	Pro	Val	Glx	Cys	Val	Pro	Lys	Lys
			20					25					30		
Arg	Gly	Met	Pro	Val	Ile	Thr	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Thr
		35					40					45			
Arg	Thr	Val	Thr	Gly	Trp	Arg	Ile	Cys	Met	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55					60				
Glu	Ala	Thr	Arg	Lys	Asp	His	Cys	Pro	Val	Pro	Phe	Ile	Asp	Gln	Met
65					70					75					80
Leu	Asp	Arg	Leu	Val	Gly	Gln	Glu	Tyr	Tyr	Cys	Phe	Leu	Glu	Gly	Tyr
				85					90					95	
Ser	Gly	Tyr	Asn	Gln	Ile	Val	Ile	Ala	Pro	Glu	Asp	Gln	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Leu	Tyr	Gly	Thr	Tyr	Ala	Phe	Lys	Glx	Leu	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Glx	Met	Met	Ala	Ile
	130					135					140				
Phe	His	Asp	Met	Val	Glu	Asp	Phe	Val	Glu	Ile	Phe	Met	Asp	Asp	Phe
145					150				155						160
Ser	Val	Phe	Arg	Glu	Ser	Phe	Asp	Arg	Cys	Leu	Glu	Asn	Trp	Asp	Arg
			165					170					175		
Val	Leu	Ala	Arg	Cys	Glu	Glu	Thr	Asn	Leu	Ile	Leu	Asn	Trp	Lys	Lys
		180						185					190		
Cys	His	Phe	Leu	Val	Asn	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser
		195					200					205			
Lys	Arg	Gly	Leu	Glu	Val	Asp	Arg	Ala	Lys	Val	Glu	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Ile	Ser	Val	Lys	Gly	Val	Arg	Ser	Phe	Leu	Gly	His
225					230					235					240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 108

<211> 761
 <212> DNA
 <213> Solanum tuberosum

<400> 108
 gtgcgtaaag aggttttcaa gctctggatg caggtattgt ctatccaatt tcagacagca 60
 agtgggtcag tccagttcag tgtgtgccta aaaagggagg catgacggtg atcactaatg 120
 aaaaaaatga gttgattcca accaggacag tgacaggatg gcgaatatgc atggattaca 180
 gaaaattaaa tgaagctacc agaaaggatc actaccgggt tccttttatt gatcagatgc 240
 tggacagggt ggctggacaa gaatattatt gtttcttgga tggttattca ggatacaacc 300
 aaatagtgat tgcaccagag gaccagggga aaactacatt cacttgcttg tatgggacat 360
 atgtttccaa gagaatgtcg tttgggctat gcaatgctcc atccattttc caaagatgca 420
 tgatggccat cttccatgat aaggttgaag attttatgga aatattcatg gatgacttct 480
 cagtatttgg ggagtctttt gacagggtgct tggagaattt agacagagtg ttggctagat 540
 gcgaggaaac taattttgtc ctaaactggg aaaaatgtca tttcctagtg aaggaagggga 600
 ttgtgttggg tcataaggtg tcaaagagag ggctggaagt tgatcgtgcc agagtggaaa 660
 taatcaaaaa gctacctccc ccaatttctg ttaaaggggt gcgaagtttt ttgggtcatg 720
 ttagtcttcta cgaaagattc ataaaggact tcaccaaggt t 761

<210> 109
 <211> 254
 <212> PRT
 <213> Solanum tuberosum

<400> 109
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Lys Trp Val Ser Pro Val Gln Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Arg Lys Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Asp His Tyr Pro Val Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Asp Arg Leu Ala Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glu Asp Gln Gly Lys Thr
 100 105 110
 Thr Phe Thr Cys Leu Tyr Gly Thr Tyr Val Ser Lys Arg Met Ser Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ser Ile Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe His Asp Lys Val Glu Asp Phe Met Glu Ile Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Gly Glu Ser Phe Asp Arg Cys Leu Glu Asn Leu Asp Arg
 165 170 175
 Val Leu Ala Arg Cys Glu Glu Thr Asn Phe Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Leu Val Lys Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Lys Arg Gly Leu Glu Val Asp Arg Ala Arg Val Glu Ile Ile Lys Lys
 210 215 220
 Leu Pro Pro Ile Ser Val Lys Gly Val Arg Ser Phe Leu Gly His
 225 230 235 240
 Val Ser Phe Tyr Glu Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 110
 <211> 762
 <212> DNA
 <213> Solanum tuberosum

<400> 110
 gtgcgtaagg aggtcctcaa gctgtctgat gcaggaattg tgtaccccat ttatgatata 60
 aagtggatca gcccagttca ctgtgtgccg aaaaagggag gcatgacgat tattactaat 120
 gaaaagaagg agttgatttc agctagaacg gtgatagagt ggcacatatg aatggactat 180
 aggagactaa atgaggcaac tagaaaggaa cactacccag ttccctttcat tgatcaaagt 240
 ttggacaggt ttattgggca agagtattat tgtttcctag atggctattc aggatataat 300
 caaattgtga ttgcgccata agataaagag aaaactacat ttacttctct atatgggaca 360
 tatgccttca agagaatgtc gtttggggccg tgcaatgctc caaccacatt ccaaagatgc 420
 atgacagcca tttttcatga tatgggtcaaa tattttgtgg agatattcat ggatgaattc 480
 ttagtccttg gggagtcctt tgacacgtgt ctagaatatt tggacaatgt gcttgccaga 540
 tgtgaggaaa ctaatcccgt cctcaactgg gaaaaatgtc attttctagt gaagaagggg 600
 attgtactag gccacaaggt ttcagaggaa ggactggaag ttgatcgtgg aaaagtagag 660
 gtaatttaaa agctaccccc tcaagtcttc gttaaagggg tgagaagggt ccttggtcat 720
 tctaggttcg aaatgagatt cataaaagac ttcacaaaag tt 762

<210> 111
 <211> 254
 <212> PRT
 <213> Solanum tuberosum

<400> 111
 Val Arg Lys Glu Val Leu Lys Leu Ser Asp Ala Gly Ile Val Tyr Pro
 1 5 10 15
 Ile Tyr Asp Ile Lys Trp Ile Ser Pro Val His Cys Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Ile Ile Thr Asn Glu Lys Lys Glu Leu Ile Ser Ala
 35 40 45
 Arg Thr Val Ile Glu Trp His Ile Glx Met Asp Tyr Arg Arg Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Glu His Tyr Pro Val Pro Phe Ile Asp Gln Met
 65 70 75 80
 Leu Asp Arg Phe Ile Gly Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Val Ile Ala Pro Glx Asp Lys Glu Lys Thr
 100 105 110
 Thr Phe Thr Ser Leu Tyr Gly Thr Tyr Ala Phe Lys Arg Met Ser Phe
 115 120 125
 Gly Pro Cys Asn Ala Pro Thr Thr Phe Gln Arg Cys Met Thr Ala Ile
 130 135 140
 Phe His Asp Met Val Lys Tyr Phe Val Glu Ile Phe Met Asp Glu Phe
 145 150 155 160
 Leu Val Phe Gly Glu Ser Phe Asp Thr Cys Leu Glu Tyr Leu Asp Asn
 165 170 175
 Val Leu Ala Arg Cys Glu Glu Thr Asn Pro Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Leu Val Lys Lys Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Glu Glu Gly Leu Glu Val Asp Arg Gly Lys Val Glu Val Ile Glx Lys
 210 215 220
 Leu Pro Pro Gln Val Phe Val Lys Gly Val Arg Arg Phe Leu Gly His
 225 230 235 240

Ser Arg Phe Glu Met Arg Phe Ile Lys Asp Phe Thr Lys Val
245 250

<210> 112
<211> 762
<212> DNA
<213> Solanum tuberosum

<400> 112
gtgcggaagg aggttttttaa gctgctggat gcggggtattg tataccagat ttcagatagc 60
aaaggggtct acccgattta gtttgtgcct aaaaaatgca gcatgacagt gatcaccaat 120
gaaaagaatg agctgattcc aaccaggaca gtgacagggt ggccaatatg catggattat 180
atgaagttga atgaggccac cagaaaggat cactaccga ttcattttat tgatcagatg 240
ttggacaagt tagctgagta aaaatattat tgtttcttgg cttgttattc aagatacaac 300
caattttctca ttgcaccaca ggaccaggag gaaactacat tcacttgtcc ttatgggaca 360
tatgcttttca agcgaatgtc gtttgggcta tgcaatgctc caaccacctt ccaaagatgc 420
ataagggcta tctttcatga tatggttgaa gattttgtgg agatattcat ggatgacttc 480
tcagtctttg ggtagtcttt tgagagggt ctggaaaatt ttgacagggt gctggctgta 540
tgcgaggaaa ctaatttttt cctaaactgg gaaaaatgtc attttctagt gaaggaaggg 600
attgtattgg gacataaggt gtcaaagtga aggcttgaag ttgatcgtgc caaagtggaa 660
gtcgttgaaa acctaccttc cccattctct gttaaagggt tgagaagttt tttgggtcat 720
gctggtttct ataggagatt tatcaaagac ttcactaagg tt 762

<210> 113
<211> 254
<212> PRT
<213> Solanum tuberosum

<400> 113
Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Ile Val Tyr Gln
1 5 10 15
Ile Ser Asp Ser Lys Gly Val Tyr Pro Ile Glx Phe Val Pro Lys Lys
20 25 30
Cys Ser Met Thr Val Ile Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr
35 40 45
Arg Thr Val Thr Gly Trp Arg Ile Cys Met Asp Tyr Met Lys Leu Asn
50 55 60
Glu Ala Thr Arg Lys Asp His Tyr Pro Ile His Phe Ile Asp Gln Met
65 70 75 80
Leu Asp Lys Leu Ala Glu Glx Lys Tyr Tyr Cys Phe Leu Ala Cys Tyr
85 90 95
Ser Arg Tyr Asn Gln Phe Leu Ile Ala Pro Gln Asp Gln Glu Glu Thr
100 105 110
Thr Phe Thr Cys Pro Tyr Gly Thr Tyr Ala Phe Lys Arg Met Ser Phe
115 120 125
Gly Leu Cys Asn Ala Pro Thr Phe Gln Arg Cys Ile Arg Ala Ile
130 135 140
Phe His Asp Met Val Glu Asp Phe Val Glu Ile Phe Met Asp Asp Phe
145 150 155 160
Ser Val Phe Gly Glx Ser Phe Glu Arg Cys Leu Glu Asn Phe Asp Arg
165 170 175
Val Leu Ala Val Cys Glu Glu Thr Asn Phe Phe Leu Asn Trp Glu Lys
180 185 190
Cys His Phe Leu Val Lys Glu Gly Ile Val Leu Gly His Lys Val Ser
195 200 205
Lys Glx Arg Leu Glu Val Asp Arg Ala Lys Val Glu Val Val Glu Asn
210 215 220

Leu Pro Ser Pro Phe Ser Val Lys Gly Val Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 114
 <211> 793
 <212> DNA
 <213> Solanum tuberosum

<400> 114
 aacttttgtg aagtcttttaa tgaaggatgt tgtcagagaa gaagtcatca agtggctgga 60
 tacagggatt gtgtacccaa tatctgacaa taaatgggca agtccagtgc agtgtgtgcc 120
 taaaaagggg ggaatgacag ttgtgaccaa tgagaaaaat gagttgatcc ccacaagaac 180
 agtaactggg tggaggctat gcatggacta cagaaaactc aatgaagcca ccaggaagga 240
 ccactattcg gtaccgttca ttgatcaaat gttagacagg ttggctggcc aagagtatta 300
 ctgtttcctt gatggttatt caaggtataa ttagatcgtc attgcacctg aggatcaaga 360
 gaatacgaca ttcacttgcc catatggcac gtatgcattc aaacgcttgc cattcggttt 420
 gtgcaatgcc ccaaccctat ttcagagatg tatgatggca atcttccatg atatggtgga 480
 agattttgtt aaagtataca tggacgattt ctcggtgttt ggtgagtcgt tcgaactttg 540
 tttatctaata cgtgatagag ttcttactag gtgtgaggag accaatttgg tgctgaactg 600
 ggagaagtgt cactttcttg tcaagagaagg aattatgttg gggcagaaga tctccaaaag 660
 tgggctagaa gtagacaagg cgaaggtgga agtgattgag aagttgccac caccaatata 720
 agtaaagggg gtgcgaagct tccttggaca tgctgggttt tacaagaggt tcataaagga 780
 cttttcaaag gtt 793

<210> 115
 <211> 264
 <212> PRT
 <213> Solanum tuberosum

<400> 115
 Thr Phe Val Lys Ser Leu Met Lys Asp Val Val Arg Glu Glu Val Ile
 1 5 10 15
 Lys Trp Leu Asp Thr Gly Ile Val Tyr Pro Ile Ser Asp Asn Lys Trp
 20 25 30
 Ala Ser Pro Val Gln Cys Val Pro Lys Lys Gly Gly Met Thr Val Val
 35 40 45
 Thr Asn Glu Lys Asn Glu Leu Ile Pro Thr Arg Thr Val Thr Gly Trp
 50 55 60
 Arg Leu Cys Met Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp
 65 70 75 80
 His Tyr Ser Val Pro Phe Ile Asp Gln Met Leu Asp Arg Leu Ala Gly
 85 90 95
 Gln Glu Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Arg Tyr Asn Glx Ile
 100 105 110
 Val Ile Ala Pro Glu Asp Gln Glu Asn Thr Thr Phe Thr Cys Pro Tyr
 115 120 125
 Gly Thr Tyr Ala Phe Lys Arg Leu Pro Phe Gly Leu Cys Asn Ala Pro
 130 135 140
 Thr Leu Phe Gln Arg Cys Met Met Ala Ile Phe His Asp Met Val Glu
 145 150 155 160
 Asp Phe Val Lys Val Tyr Met Asp Asp Phe Ser Val Phe Gly Glu Ser
 165 170 175
 Phe Glu Leu Cys Leu Ser Asn Arg Asp Arg Val Leu Thr Arg Cys Glu
 180 185 190
 Glu Thr Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Leu Val Arg

195					200					205					
Glu	Gly	Ile	Met	Leu	Gly	Gln	Lys	Ile	Ser	Lys	Ser	Gly	Leu	Glu	Val
210					215					220					
Asp	Lys	Ala	Lys	Val	Glu	Val	Ile	Glu	Lys	Leu	Pro	Pro	Pro	Ile	Glx
225					230					235					
Val	Lys	Gly	Val	Arg	Ser	Phe	Leu	Gly	His	Ala	Gly	Phe	Tyr	Lys	Arg
245					250					255					
Phe	Ile	Lys	Asp	Phe	Ser	Lys	Val								
260															

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<210> 116
<211> 761
<212> DNA
<213> Platanus occidentalis
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<400>	116						
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tagaatgatg	agttgggtcc	taccagtgtt	cagaatgggt	ggaggggttg	atagattata		180
gaaaattgaa	tggtgtaacc	cgcaaggatc	acttcacctt	accttttatt	gatcaaatgc		240
ttgaaagggt	agttgggtcat	tcttactatt	gtttcctaga	tggttattca	agttatttcc		300
agattgtaat	tactccagag	gattaagaaa	agacaacctt	tacatgtcca	tttgggactt		360
ttgcatatcg	ttgcatgccc	tttggccctt	gcaatgcccc	aaccactttc	caaaggtgta		420
tggttagcat	attttcatat	tacattgaga	atatcataga	agtttttatg	gatgatttca		480
tagtttatgg	agactccttt	aataattttc	tgcataacct	tacatttgtt	cttcaaagat		540
gcatagaaac	taaccttgtg	ttaaattatg	aaaaatgtca	ttttatgggt	gaacaaggta		600
tagttttggg	tcatgcttatt	tcatctaaag	gaattgaggt	agataaagct	aaagttgata		660
ttattcaatc	tttatcttat	ctcattagta	tgcggaaggt	tcattccttt	cttggacatg		720
cagqtttcta	ccqaagattc	attaaagact	ttacaaaggt	t			761

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<210> 117
<211> 254
<212> PRT
<213> Platanus occidentalis
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<400>	117														
Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	Lys	Val	Glx	Val	Ile	Tyr	Pro
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Ile	Glx	Asp	Arg	Asn	Trp	Val	Ser	Pro	Val	Gln	Val	Val	Pro	Lys	Lys
			20					25					30		
Ile	Gly	Ile	Thr	Val	Val	Lys	Asn	Glx	Asn	Asp	Glu	Leu	Val	Pro	Thr
		35					40					45			
Ser	Val	Gln	Asn	Gly	Trp	Arg	Val	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55					60				
Val	Val	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met
65					70					75					80
Leu	Glu	Arg	Leu	Val	Gly	His	Ser	Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr
				85					90					95	
Ser	Ser	Tyr	Phe	Gln	Ile	Val	Ile	Thr	Pro	Glu	Asp	Glx	Glu	Lys	Thr
			100					105					110		
Thr	Phe	Thr	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	Cys	Met	Pro	Phe
			115				120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Gln	Arg	Cys	Met	Val	Ser	Ile
	130					135					140				
Phe	Ser	Tyr	Tyr	Ile	Glu	Asn	Ile	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Ile	Val	Tyr	Gly	Asp	Ser	Phe	Asn	Asn	Phe	Leu	His	Asn	Leu	Thr	Leu

Val	Leu	Gln	Arg	Cys	Ile	Glu	Thr	Asn	Leu	Val	Leu	Asn	Tyr	Glu	Lys
			180					185					190		
Cys	His	Phe	Met	Val	Glu	Gln	Gly	Ile	Val	Leu	Gly	His	Val	Ile	Ser
		195					200					205			
Ser	Lys	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Val	Asp	Ile	Ile	Gln	Ser
		210				215					220				
Leu	Pro	Tyr	Leu	Ile	Ser	Met	Arg	Lys	Val	His	Ser	Phe	Leu	Gly	His
225					230					235					240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

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<210> 118
<211> 762
<212> DNA
<213> Platanus occidentalis
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[illegible]

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<210> 119
<211> 254
<212> PRT
<213> Platanus occidentalis
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<400> 119															
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Ile	Ser	Asn	Ser	Asn	Trp	Val	Ser	Pro	Val	Gln	Val	Ala	Pro	Lys	Lys
			20					25					30		
Thr	Gly	Ile	Thr	Val	Val	Lys	Asn	Gln	Asn	Asp	Glu	Leu	Val	Pro	Thr
		35					40					45			
His	Val	Gln	Asn	Gly	Trp	Trp	Val	Cys	Ile	Asn	Tyr	Arg	Lys	Leu	Asn
	50					55					60				
Val	Ile	Thr	Cys	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Lys	Met
65					70					75					80
Leu	Glu	Arg	Leu	Ala	Gly	His	Ser	Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr
				85					90					95	
Leu	Gly	Tyr	Phe	Gln	Ile	Ala	Ile	Thr	Ser	Glu	Asp	Gln	Glu	Lys	Met
			100					105					110		
Ile	Phe	Lys	Cys	Pro	Phe	Gly	Thr	Phe	Ala	Tyr	Arg	His	Met	Pro	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Glx	Arg	Cys	Met	Val	Ser	Ile
	130					135					140				
Phe	Ser	Asp	Tyr	Ile	Glu	Asn	Ile	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe

145		150		155		160
Thr Val Tyr Gly Asp	Ser Phe Asp Asn Cys Leu His Asn Leu Thr Leu					
	165		170		175	
Val Ile Gln Arg Cys	Ile Glu Thr Asn Leu Val Leu Asn Ser Glx Lys					
	180		185		190	
Cys His Phe Met Val	Glu Gln Gly Ile Val Leu Gly His Val Val Ser					
	195		200		205	
Ser Arg Gly Ile Glu	Val Asp Lys Pro Lys Val Asp Ile Ile Gln Thr					
	210		215		220	
Leu Pro Tyr Ser Thr	Ser Val Arg Glu Val Arg Ser Phe Leu Gly His					
225		230		235		240
Val Gly Phe Tyr Glx	Arg Phe Ile Lys Asp Phe Thr Lys Val					
	245		250			

<210> 120

<211> 759

<212> DNA

<213> Platanus occidentalis

<400> 120

gtgcggaag	agggttttaa	gcttttggat	gtagggatta	tatacccaat	tttttatagt	60
aattaggtaa	gtccactca	agtggacca	agaattctgg	tgtgactgta	gttaaaaatg	120
caaagtatga	attgattcca	aatagactca	ctattgggtg	gcgtgtatgc	attaactata	180
agaagttgaa	ctcagtgact	aggaaggacc	atttcccttt	accattcatg	actaaatcct	240
agaaagggtg	gctggtcaca	aattttatta	tttccctatat	ggttattcta	gatataacta	300
aatagagatt	gcacctgagg	actaagaaaa	taccactttt	acatgtccat	ttggcacttt	360
tgcttatcga	aggatgtcat	ttggattatg	taatgctctt	gccacgttct	aaagatgcat	420
gttgagtata	tttagtgata	tggtagaaca	ttttcttgag	gtgtttatgg	attttttttg	480
tttttggtaa	ttcatttgat	gattgtttgc	ataatttgaa	aaaagtgtta	aatagatgtg	540
aaggaaaaaa	acatcatttt	gaattgagag	aagtgtcatt	tcatggcttc	taaaagaatt	600
gtacttggtc	acattgtctc	ctcccaagga	attaaagtgg	tcaaagccaa	aattgaattg	660
atagtcaatt	tgccatgccc	aaagactctt	aaagacattc	gatcttttct	aggatcatgca	720
ggatttaaca	aaaggttcat	caaagacttc	acgaaagtt			759

<210> 121

<211> 254

<212> PRT

<213> Platanus occidentalis

<400> 121

Val Arg Lys Glu Val	Phe Lys Leu Leu Asp Val	Gly Ile Ile Tyr Pro
1	5	10
Ile Phe Tyr Ser Asn	Glx Val Ser Pro Thr	Gln Val Val Pro Lys Asn
	20	25
Ser Gly Val Thr Val	Val Lys Asn Ala Asn Asp	Glu Leu Ile Pro Asn
	35	40
Arg Leu Thr Ile Gly	Trp Arg Val Cys Ile Asn	Tyr Lys Lys Leu Asn
	50	55
Ser Val Thr Arg Lys	Asp His Phe Pro Leu Pro	Phe Met Asp Glx Ile
	65	70
Leu Glu Arg Val Ala	Gly His Lys Phe Tyr Tyr	Phe Leu Tyr Gly Tyr
	85	90
Ser Arg Tyr Asn Glx	Ile Glu Ile Ala Pro Glu	Asp Glx Glu Asn Thr
	100	105
Thr Phe Thr Cys Pro	Phe Gly Thr Phe Ala Tyr	Arg Arg Met Ser Phe
	115	120
Gly Leu Cys Asn Ala	Leu Ala Thr Phe Glx	Arg Cys Met Leu Ser Ile
		125

130	135	140
Phe Ser Asp Met Val Glu His Phe Leu Glu Val Phe Met Asp Asp Phe		
145	150	155
Phe Val Phe Gly Asn Ser Phe Asp Asp Cys Leu His Asn Leu Lys Lys		160
	165	170
Val Leu Asn Arg Cys Glu Glu Lys Asn Ile Ile Leu Asn Glx Glu Lys		175
	180	185
Cys His Phe Met Val Ser Lys Arg Ile Val Leu Gly His Ile Val Ser		190
	195	200
Ser Gln Gly Ile Lys Val Val Lys Ala Lys Ile Glu Leu Ile Val Asn		205
	210	215
Leu Pro Ser Pro Lys Thr Leu Lys Asp Ile Arg Ser Phe Leu Gly His		220
225	230	235
Ala Gly Phe Asn Lys Arg Phe Ile Lys Asp Phe Thr Lys Val		240
	245	250

<210> 122
 <211> 761
 <212> DNA
 <213> Platanus occidentalis

<400> 122	
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attggggttag cccggttcaa gtggttccta aaaagactgg aataaccgtt gtgaaaaatc	120
aaaatgatga gttagtctcct acccgtgttc agaatgggtg gcaggtttgt atagattata	180
taaaattaaa tggtgtaacc cgcaaggatc acttcccttt accttttatt gatcaaagt	240
ttgaaagggt agctggtcat tcttactatt gtttccttga tggatattca tgttattttt	300
agattgcaat tactccagag gatcaagaaa agacgacttt tacgtgccca ttcgggactt	360
tttcatatcg ttgcatgccc tttggccttt gcaacgcccc agccactttc caaagggtga	420
tggttagcat attttcagat tacattgaga atatcataga agtcctttatg gatgatttca	480
tagtttatga agactccttt gataattgtc tgcataacct tacacttggt ttttaaagat	540
gcatagaaac taaccttggtg ttaaattttg aaaaatgtca tgttatgggt gaataaggta	600
tagttttggg tcatgttggt tcatctatgg gaattgaggt agataaagtt aaagttgata	660
ttattcaatc tttaccttat cccattagtg tgcaggaagt tcgttctttt cttggacatg	720
cgggttttta ccaaagattc attaaagact tcacgaaagt t	761

<210> 123
 <211> 253
 <212> PRT
 <213> Platanus occidentalis

<400> 123	
Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Val Ile Tyr Pro Ile	
1	15
Ser Asp Ser Asn Trp Val Ser Pro Val Gln Val Val Pro Lys Lys Thr	
20	30
Gly Ile Thr Val Val Lys Asn Gln Asn Asp Glu Leu Val Pro Thr Arg	
35	45
Val Gln Asn Gly Trp Gln Val Cys Ile Asp Tyr Ile Lys Leu Asn Val	
50	60
Val Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met Phe	
65	80
Glu Arg Leu Ala Gly His Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser	
85	95
Cys Tyr Phe Glx Ile Ala Ile Thr Pro Glu Asp Gln Glu Lys Thr Thr	
100	110
Phe Thr Cys Pro Phe Gly Thr Phe Ser Tyr Arg Cys Met Pro Phe Gly	

115 120 125
 Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Val Ser Ile Phe
 130 135 140
 Ser Asp Tyr Ile Glu Asn Ile Ile Glu Val Phe Met Asp Asp Phe Ile
 145 150 155 160
 Val Tyr Glu Asp Ser Phe Asp Asn Cys Leu His Asn Leu Thr Leu Val
 165 170 175
 Phe Glx Arg Cys Ile Glu Thr Asn Leu Val Leu Asn Phe Glu Lys Cys
 180 185 190
 His Val Met Val Glu Glx Gly Ile Val Leu Gly His Val Val Ser Ser
 195 200 205
 Met Gly Ile Glu Val Asp Lys Val Lys Val Asp Ile Ile Gln Ser Leu
 210 215 220
 Pro Tyr Pro Ile Ser Val Gln Glu Val Arg Ser Phe Leu Gly His Ala
 225 230 235 240
 Gly Phe Tyr Gln Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 124
 <211> 761
 <212> DNA
 <213> Sorghum bicolor

<400> 124
 gtgcgtaaaag aggtcttcaa gctctatcat gctgggatta tttatcctgt gccgcatagt 60
 gagtgggtta gccctgttca agtagtgcca aagaaaggag gaatgacggt cgtaggaat 120
 gagaagaatg aactcatccc tcaacgaatt gtcactgggt ggcgtatgtg tattgactat 180
 caaaaactca acacggctac aaagaaagat aactttccgt tacccttcat tgatgaaatg 240
 ttggaacggc ttgcaaacca ctctttcttc tgtttccttg atggttattc tggatatcac 300
 caaatcccaa tccaccaga tgaccaagaa aagactacct ttacatgccc gtatggaact 360
 tatgcataac gacgaatgtc gttcggactg tgcaatgtc cagcttcttt ccaacgggtgc 420
 atgatgtcta ttttctcgga catgattgag aagatcatgg aggttttcat ggatgatttt 480
 accgtctatg gtaaaacctt cgatcattgt ttggagaatt tagatagagt cttgcagcga 540
 tgtgaagaaa agcacttaat cctgaactgg gagaaatgcc attttatggt tcaggaagga 600
 atagtgttag gacataaagt gtccgaacgt ggtatagagg tggacaaagc aaagattgaa 660
 gttattgaaa aacttccacc tcccacgaat gtgaaaggat ccgtagcttc ttgggacatg 720
 cagggttcta tagatgcttc ataaaagact tcacaaagggt t 761

<210> 125
 <211> 254
 <212> PRT
 <213> Sorghum bicolor

<400> 125
 Val Arg Lys Glu Val Phe Lys Leu Tyr His Ala Gly Ile Ile Tyr Pro
 1 5 10 15
 Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Val Arg Asn Glu Lys Asn Glu Leu Ile Pro Gln
 35 40 45
 Arg Ile Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
 50 55 60
 Thr Ala Thr Lys Lys Asp Asn Phe Pro Leu Pro Phe Ile Asp Glu Met
 65 70 75 80
 Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Glu Lys Thr

				100					105					110		
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Glx	Arg	Arg	Met	Ser	Phe	
			115				120					125				
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile	
		130				135					140					
Phe	Ser	Asp	Met	Ile	Glu	Lys	Ile	Met	Glu	Val	Phe	Met	Asp	Asp	Phe	
145					150					155					160	
Thr	Val	Tyr	Gly	Lys	Thr	Phe	Asp	His	Cys	Leu	Glu	Asn	Leu	Asp	Arg	
				165					170					175		
Val	Leu	Gln	Arg	Cys	Glu	Glu	Lys	His	Leu	Ile	Leu	Asn	Trp	Glu	Lys	
			180					185					190			
Cys	His	Phe	Met	Val	Gln	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser	
		195					200					205				
Glu	Arg	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Ile	Glu	Val	Ile	Glu	Lys	
		210				215					220					
Leu	Pro	Pro	Pro	Thr	Asn	Val	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His	
225					230					235					240	
Ala	Gly	Phe	Tyr	Arg	Cys	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val			
				245					250							

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<210> 126
<211> 762
<212> DNA
<213> Sorghum bicolor
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[illegible]

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<210> 127
<211> 254
<212> PRT
<213> Sorghum bicolor
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<400> 127															
Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	His	Ala	Gly	Ile	Ile	Tyr	Pro
1				5					10					15	
Val	Pro	His	Ser	Glu	Trp	Val	Ser	Pro	Val	Gln	Val	Val	Pro	Lys	Lys
			20					25					30		
Gly	Gly	Met	Thr	Val	Ile	Ile	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Gln
		35					40					45			
Arg	Thr	Val	Thr	Gly	Trp	Gln	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55					60				
Lys	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Glu	Met
65					70					75				80	
Leu	Glu	Arg	Leu	Ala	Asn	His	Ser	Phe	Phe	Cys	Phe	Leu	Asp	Gly	Tyr

				85					90					95			
Ser	Gly	Tyr	His	Gln	Ile	Pro	Ile	His	Pro	Asp	Asp	Gln	Ser	Lys	Thr		
			100					105					110				
Thr	Phe	Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	Arg	Arg	Met	Ser	Phe		
		115					120					125					
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile		
		130				135					140						
Phe	Ser	Asp	Met	Ile	Glu	Glu	Ile	Met	Glu	Val	Phe	Met	Asp	Asp	Phe		
145				150					155						160		
Ser	Val	Tyr	Gly	Lys	Ala	Phe	Asp	Ser	Cys	Leu	Glu	Asn	Leu	Asp	Lys		
			165				170							175			
Val	Leu	Gln	Ser	Cys	Glu	Glu	Lys	His	Leu	Ile	Leu	Asn	Trp	Glu	Lys		
		180					185						190				
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Leu	Val	Ser		
	195					200					205						
Glu	Arg	Gly	Ile	Glu	Val	Asp	Lys	Ala	Glu	Ile	Glu	Val	Ile	Glu	Gln		
	210					215					220						
Leu	Pro	Pro	Pro	Val	Asn	Ile	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His		
225				230					235						240		
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val				
			245					250									

<210> 128
 <211> 762
 <212> DNA
 <213> Sorghum bicolor

<400> 128																	
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gagtggggta	gcacgggtaca	agttgtgcc	aagaaaggag	gaatgtcggg	tgtaggaat											120	
gagaagaacg	aattcatccc	tcaacaaact	gtcactgggt	ggcgtatgtg	cattgactac											180	
caaaaactca	acaaggccac	aaggaaagat	cacttcccgt	tacctttcat	tgatgaaatg											240	
ttgtaatggc	ttacaaatca	ctcgttcttt	tgtttccttg	aagggtattc	cagatatcat											300	
caaatcccga	tccaccacga	tgaccaaaagt	aagactactt	tcacatgacc	ctatggaact											360	
tacgcatacc	gacgaatgtc	gttcagggtta	tgtaatgctc	cagcttcttt	tcaacgggtgc											420	
atgatgtcta	ttttttccaa	tatgattgag	aaaatcatgg	aggtattcac	ggatgatttt											480	
accgtatatg	gcaaaacctt	tgatgattgt	ttagagaatt	tggaacaaagt	cttacaattg											540	
tgtgaaggaa	agcacttaat	cgtaaaactag	gagaaatgcc	attttatggg	ccgagaagga											600	
atagtgtctag	ggcacaaggt	gtccgaacgt	gggatagagg	tggaatagagc	caagattgaa											660	
gttattgaaa	aacttccacc	tcccacaaat	gtgaaagaca	tccgcagttt	tcttggacat											720	
gcagggttct	ataggcgctt	catcaaagat	ttcaccaagg	tt												762	

<210> 129
 <211> 254
 <212> PRT
 <213> Sorghum bicolor

<400> 129																	
Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	His	Thr	Arg	Ile	Ile	Tyr	Leu		
1				5					10					15			
Val	Pro	His	Ser	Glu	Trp	Val	Ser	Thr	Val	Gln	Val	Val	Pro	Lys	Lys		
			20					25					30				
Gly	Gly	Met	Ser	Val	Val	Arg	Asn	Glu	Lys	Asn	Glu	Phe	Ile	Pro	Gln		
		35				40					45						
Gln	Thr	Val	Thr	Gly	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Gln	Lys	Leu	Asn		
	50				55					60							
Lys	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Glu	Met		

65					70						75				80
Leu	Glx	Trp	Leu	Thr	Asn	His	Ser	Phe	Phe	Cys	Phe	Leu	Glu	Gly	Tyr
				85					90					95	
Ser	Arg	Tyr	His	Gln	Ile	Pro	Ile	His	His	Asp	Asp	Gln	Ser	Lys	Thr
			100					105				110			
Thr	Phe	Thr	Glx	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	Arg	Arg	Met	Ser	Phe
		115					120					125			
Arg	Leu	Cys	Asn	Ala	Pro	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile
	130					135					140				
Phe	Ser	Asn	Met	Ile	Glu	Lys	Ile	Met	Glu	Val	Phe	Thr	Asp	Asp	Phe
145					150				155						160
Thr	Val	Tyr	Gly	Lys	Thr	Phe	Asp	Asp	Cys	Leu	Glu	Asn	Leu	Asp	Lys
			165						170					175	
Val	Leu	Gln	Leu	Cys	Glu	Gly	Lys	His	Leu	Ile	Val	Asn	Glx	Glu	Lys
		180						185					190		
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Val	Ser
		195					200					205			
Glu	Arg	Gly	Ile	Glu	Val	Asp	Arg	Ala	Lys	Ile	Glu	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Thr	Asn	Val	Lys	Asp	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230				235						240
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 130

<211> 761

<212> DNA

<213> Sorghum bicolor

<400> 130

gtgcgtaagg	aggttttttaa	gctgctgcat	gcagagatta	tatatcatgt	gccgcacagt	60
gagtgggttaa	gcccagttca	agttgtgcct	aaaaagggag	gcatgattgt	tgttacgaat	120
gaaaagaacg	agctaattcc	gcaacgcacc	gtcacagggt	ggcggatgtg	catagactat	180
agaaaactaa	acaaagccac	gagaaaggat	cattttcctt	tacctttcat	agatgagatg	240
ctagagcgat	tagcaaacca	ttcgttcttc	tgtttcttag	atggataatt	agggtatcac	300
cagatcccaa	tcaatcttga	tgatcaaagc	aaaaccactt	ttccatgccc	acatggaact	360
tatgcttacc	gtagaatgtc	ttttgggtta	tgtaatgcac	cagcttcttt	tcaaagatgc	420
atgatgtctg	tattttctaa	tatgattgaa	gagattatgg	aattttcatg	gatgatttct	480
ctgtttatgg	aaaaactttt	gatagttgtc	ttgaaaactt	agacagggtt	ttgcaaagat	540
gtgaagaaaa	gtacttagtc	cttaattgga	aaaaatgtca	ttttatgggt	aggggaaggaa	600
tagtgctggg	acacctagtg	tctgaaagag	gtattgaggt	cgacaaagct	aaaattgaag	660
taattgaaca	actacctcca	cctttgaata	taaaaggaat	tcgaagcttt	cttggccatg	720
ctgggttttta	tcgtagattc	attaaggact	ttacaaaggt	t		761

<210> 131

<211> 254

<212> PRT

<213> Sorghum bicolor

<400> 131

Val	Arg	Lys	Glu	Val	Phe	Lys	Leu	Leu	His	Ala	Glu	Ile	Ile	Tyr	His
1				5					10					15	
Val	Pro	His	Ser	Glu	Trp	Val	Ser	Pro	Val	Gln	Val	Val	Pro	Lys	Lys
		20					25					30			
Gly	Gly	Met	Ile	Val	Val	Thr	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Gln
	35					40					45				
Arg	Thr	Val	Thr	Gly	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn

50		55		60	
Lys Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met					
65		70		75	80
Leu Glu Arg Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Glx					
	85		90		95
Leu Gly Tyr His Gln Ile Pro Ile Asn Leu Asp Asp Gln Ser Lys Thr					
	100		105		110
Thr Phe Pro Cys Pro His Gly Thr Tyr Ala Tyr Arg Arg Met Ser Phe					
	115		120		125
Gly Leu Cys Asn Ala Pro Ala Ser Phe Gln Arg Cys Met Met Ser Val					
	130		135		140
Phe Ser Asn Met Ile Glu Ile Met Glu Ile Phe Met Asp Asp Phe					
145		150		155	160
Ser Val Tyr Gly Lys Thr Phe Asp Ser Cys Leu Glu Asn Leu Asp Arg					
	165		170		175
Val Leu Gln Arg Cys Glu Glu Lys Tyr Leu Val Leu Asn Trp Lys Lys					
	180		185		190
Cys His Phe Met Val Arg Glu Gly Ile Val Leu Gly His Leu Val Ser					
	195		200		205
Glu Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Glu Val Ile Glu Gln					
	210		215		220
Leu Pro Pro Pro Leu Asn Ile Lys Gly Ile Arg Ser Phe Leu Gly His					
225		230		235	240
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val					
	245		250		

<210> 132
 <211> 763
 <212> DNA
 <213> Sorghum bicolor

<400> 132					60
gtgcggaaag aggtcgtcaa gctctatcat gctgggatta tttatcctgt gccacatagt					120
gagtgggtta gccctgttca agtagtgcca aagaaagaag gaatgacggt cgtaggaat					180
gagaagaatg aactcatccc tcaacaaatt gtcactagat ggcgtatgtg tattgactat					240
cgaaaactca acaaagctac aaagaaagat cactttccgt tacccttcat tgatgaaatg					300
ttggaatggc ttgcaaacca ctctttcttc tgtttccttg atggttattc tggatatcac					360
caaatcccaa tccaccaga tgaccaagaa aagactacct ttacatgccc gtattgaact					420
tatgcatact gacgaatgtc gttcggattg tgcaatgtc tagcttcttt tccagcggtg					480
catgatgtct attttctcgg acatgattga gaagatcatg gaggttttca tggatgattt					540
taccgtctat ggcaaaacct tcgatcattg tttggagaat ttagatagag tcttgcagcg					600
atgtgaggaa aatcacttaa tcttgaactg ggagaaatgt cattttatgg ttcaggaagg					660
aatagtgcta ggacataaag tgtccgaacg tggatatagat gtggacaaaag caaagattaa					720
agttattgaa aaacttccac ctcacacgaa tgtgaaagga atccatagct ttttgggaca					763
tgcagggttc tatagacgct tcatcaagga tttcacaaag gtt					

<210> 133
 <211> 254
 <212> PRT
 <213> Sorghum bicolor

<400> 133					
Val Arg Lys Glu Val Val Lys Leu Tyr His Ala Gly Ile Ile Tyr Pro					
1	5		10		15
Val Pro His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys					
	20		25		30
Glu Gly Met Thr Val Val Arg Asn Glu Lys Asn Glu Leu Ile Pro Gln					

35	40	45
Gln Ile Val Thr Arg Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn		
50	55	60
Lys Ala Thr Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Glu Met		
65	70	75
Leu Glu Trp Leu Ala Asn His Ser Phe Phe Cys Phe Leu Asp Gly Tyr		
85	90	95
Ser Gly Tyr His Gln Ile Pro Ile His Pro Asp Asp Gln Glu Lys Thr		
100	105	110
Thr Phe Thr Cys Pro Tyr Glx Thr Tyr Ala Tyr Glx Arg Met Ser Phe		
115	120	125
Gly Leu Cys Asn Ala Leu Ala Ser Phe Gln Arg Cys Met Met Ser Ile		
130	135	140
Phe Ser Asp Met Ile Glu Lys Ile Met Glu Val Phe Met Asp Asp Phe		
145	150	155
Thr Val Tyr Gly Lys Thr Phe Asp His Cys Leu Glu Asn Leu Asp Arg		
165	170	175
Val Leu Gln Arg Cys Glu Glu Asn His Leu Ile Leu Asn Trp Glu Lys		
180	185	190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Val Ser		
195	200	205
Glu Arg Gly Ile Asp Val Asp Lys Ala Lys Ile Lys Val Ile Glu Lys		
210	215	220
Leu Pro Pro His Thr Asn Val Lys Gly Ile His Ser Phe Leu Gly His		
225	230	235
Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val		
245	250	

<210> 134
 <211> 756
 <212> DNA
 <213> Sorghum bicolor

<400> 134	
aaggaggttt tcaagttgct gcatgcaggg attatatatc ttgtgccgca tagtgagtgg	60
gtaagcccag ttcaagttgt gcctaaaaag ggaggcatga ctattattat gaatgaaaag	120
aacgagctaa ttccgcaacg caccgttaca gtatggcgga tgtgcataga ctatagaaaa	180
ctaaacaaaag ccacgagaga ggatcacttt cctttacctt tcatagatga gatgctagag	240
tggttagcaa accattcggt cttctgtttc ttagatggat attgagggtta tcatcagatc	300
ccgatccatc ccgatgatca aagcaaaacc acttttacat gcccatatgg aacttatgct	360
taccgtagaa tgtcttttgg gttatgtaat gcactagctt cttttcaaag atgcatgatg	420
tctatatttt ctgatatgat tgaagagatt atggaagttt tcatggatga tttctctggt	480
tatggaaaaa cttttgatag ttgtcttaaa aacttagaca aggttttgca aagatgtgaa	540
gaaaagcact tagtccttaa ttgggaaaaa tgtcatttca tgggttaggga aggaatagtg	600
ctgggacact tagtgtctga aagagctatt gaggtagata aagctaaaaa tgaagtaatt	660
gaacaactac gtccacctgt gaacataaaa ggaatttgaa gctttcttgg ccatgctggt	720
tttcatcgta gattcataaa agactttaca aaggtt	756

<210> 135
 <211> 252
 <212> PRT
 <213> Sorghum bicolor

<400> 135
Lys Glu Val Phe Lys Leu Leu His Ala Gly Ile Ile Tyr Leu Val Pro
1 5 10 15
His Ser Glu Trp Val Ser Pro Val Gln Val Val Pro Lys Lys Gly Gly

			20				25					30			
Met	Thr	Ile	Met	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Gln	Arg	Thr	
		35				40					45				
Val	Thr	Val	Trp	Arg	Met	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn	Lys	Ala
	50					55					60				
Thr	Arg	Glu	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Glu	Met	Leu	Glu
65					70					75					80
Trp	Leu	Ala	Asn	His	Ser	Phe	Phe	Cys	Phe	Leu	Asp	Gly	Tyr	Glx	Gly
				85				90						95	
Tyr	His	Gln	Ile	Pro	Ile	His	Pro	Asp	Asp	Gln	Ser	Lys	Thr	Thr	Phe
			100					105					110		
Thr	Cys	Pro	Tyr	Gly	Thr	Tyr	Ala	Tyr	Arg	Arg	Met	Ser	Phe	Gly	Leu
		115					120					125			
Cys	Asn	Ala	Leu	Ala	Ser	Phe	Gln	Arg	Cys	Met	Met	Ser	Ile	Phe	Ser
	130					135					140				
Asp	Met	Ile	Glu	Glu	Ile	Met	Glu	Val	Phe	Met	Asp	Asp	Phe	Ser	Val
145					150					155					160
Tyr	Gly	Lys	Thr	Phe	Asp	Ser	Cys	Leu	Lys	Asn	Leu	Asp	Lys	Val	Leu
				165					170					175	
Gln	Arg	Cys	Glu	Glu	Lys	His	Leu	Val	Leu	Asn	Trp	Glu	Lys	Cys	His
			180					185					190		
Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Leu	Val	Ser	Glu	Arg
		195					200					205			
Ala	Ile	Glu	Val	Asp	Lys	Ala	Lys	Ile	Glu	Val	Ile	Glu	Gln	Leu	Arg
	210					215					220				
Pro	Pro	Val	Asn	Ile	Lys	Gly	Ile	Glx	Ser	Phe	Leu	Gly	His	Ala	Gly
225					230					235					240
Phe	His	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val				
				245					250						

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<210> 136
<211> 762
<212> DNA
<213> Glycine max
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<400> 136																							
gtg	cgt	aa	agg	tgt	caa	gct	ttt	tgg	gag	gtt	ggg	gct	ca	tata	cct	cat	ctc	tg	ac	ag	c	60	
gct	tgg	gta	a	gc	ctag	taca	ggt	ggc	tccc	aag	aa	tgc	g	ga	atg	ac	agt	ggt	ac	aaa	aat	120	
gag	agga	aatg	a	act	tga	tacc	aac	ac	ga	act	gtc	act	ggc	agc	gg	atg	tgt	tat	cga	ctac		180	
tg	ca	agt	tga	at	ga	agcc	ac	gga	agg	gac	catt	tcccc	t	tac	ctt	tcc	at	gg	atc	ag	atg	240	
ct	gg	ag	agg	c	ttg	caggg	ca	gg	cat	act	tac	tg	ttt	ctt	gg	at	at	ag	gata	ca	aac	300	
caa	atc	gc	g	g	tag	acccc	ag	at	cagg	gag	aag	atg	ggc	ct	cat	gccc	ctt	tgg	cgc	t		360	
ttt	gct	taca	ga	agg	atg	t	att	cagg	tta	tgt	aac	gc	ac	ca	gcc	ac	att	cag	agg	tgc		420	
gtg	ctg	ggcca	ttt	ttt	t	caga	cat	gg	tgg	gag	aag	ag	cat	c	g	at	tt	gga	tga	att	c	480	
tcg	att	ttt	tg	gacc	ctt	tatt	tg	ac	agt	tgc	tta	agg	aa	ct	tag	ag	at	g	at	g	g	540	
tg	cgt	ataga	cta	act	tgg	t	ct	aa	att	ag	g	aaaa	aat	gtc	att	t	cat	gg	t	cga	gag	ggga	600
atag	tga	tga	acc	aca	aat	at	c	t	cag	ctaga	ggg	att	gag	g	tt	gat	cagg	c	aa	ga	tag	ac	660
gtc	att	tgaga	agt	t	gcc	acc	acc	act	ga	aat	gtt	aa	agg	gc	t	caga	ag	ttt	ctt	agg	gc	at	720
qc	agg	ttt	ct	ac	agg	aggt	t	at	ca	agg	ac	tt	ca	cc	a	agg	tt						762

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<210> 137
<211> 254
<212> PRT
<213> Glycine max
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<400> 137
Val Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Leu Ile Tyr Leu

1	5	10	15
Ile Ser Asp	Ser Ala Trp Val Ser	Leu Val Gln Val Ala Pro	Lys Lys
	20	25	30
Cys Gly Met	Thr Val Val Gln Asn Glu Arg Asn Asp	Leu Ile Pro Thr	
35	40	45	
Arg Thr Val	Thr Gly Glx Arg Met Cys Ile Asp Tyr Cys Lys Leu Asn		
50	55	60	
Glu Ala Thr	Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met		
65	70	75	80
Leu Glu Arg	Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Arg Tyr		
	85	90	95
Ser Gly Tyr	Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Met		
	100	105	110
Ala Phe Thr	Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Ser Phe		
	115	120	125
Arg Leu Cys	Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Leu Ala Ile		
130	135	140	
Phe Ser Asp	Met Val Glu Lys Ser Ile Glu Val Phe Met Asp Glu Phe		
145	150	155	160
Ser Ile Phe	Gly Pro Leu Phe Asp Ser Cys Leu Arg Asn Leu Glu Met		
	165	170	175
Val Leu Gln	Arg Cys Val Glx Thr Asn Leu Val Leu Asn Glx Glu Lys		
	180	185	190
Cys His Phe	Met Val Arg Glu Gly Ile Val Met Asp His Asn Ile Ser		
	195	200	205
Ala Arg Gly	Ile Glu Val Asp Gln Ala Lys Ile Asp Val Ile Glu Lys		
210	215	220	
Leu Pro Pro	Pro Leu Asn Val Lys Gly Val Arg Ser Phe Leu Gly His		
225	230	235	240
Ala Gly Phe	Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val		
	245	250	

<210> 138
 <211> 763
 <212> DNA
 <213> Glycine max

<400> 138	
gtgcgtaagg aggtcttttaa gttcttggag gctgggctca tatatcccat ctctaatagc	60
acttaggttaa gccaggtaca ggtggttccc aagaaagggtg gaatgacagt agtacagaat	120
gagaagaatg acttgatacc aacacgaact gtcactagct ggccaatatg catcgattat	180
cgcaagctga atgaggccac ccggaaggac cacttccctc tacctttcat ggatcagatg	240
ttggagagac ttgcagggca ggcgtattat tgtttcttgg atggatactc gagatataat	300
cagattgcgg tggaccctag agaccaagag aagacgacct tcacatgccc tttttggcgt	360
ctttgcttac agaaggatgc cattcgggtt atgtaatgca ccagccacat ttcagagggtg	420
catgctggcc attttttcag acatggtgga gaaaaatata gaggtattca tggatgactt	480
ttcagttttt gggccctcat ttgacagttg tttgaggaac cttagagatgg tacttttagag	540
gtgcgtagag actaatatag tgctgaactg ggagaagtgt cattttatgg ttcgagaggg	600
catagtccctg agccacaaga tctcagctag agggattgag gttgaccggg caaagataga	660
cgctatagag aagctgccac caccattgaa tattaaaggt gtcagaagtt tcttagggca	720
tgcaggattc tacaggagat tcataaagga ctttacaaag gtt	763

<210> 139
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 139

Val Arg Lys Glu Val Phe Lys Phe Leu Glu Ala Gly Leu Ile Tyr Pro
 1 5 10 15
 Ile Ser Asn Ser Thr Glx Val Ser Pro Val Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Val Gln Asn Glu Lys Asn Asp Leu Ile Pro Thr
 35 40 45
 Arg Thr Val Thr Ser Trp Arg Ile Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Glu Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly Gln Ala Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Arg Tyr Asn Gln Ile Ala Val Asp Pro Arg Asp Gln Glu Lys Thr
 100 105 110
 Thr Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Leu Ala Ile
 130 135 140
 Phe Ser Asp Met Val Glu Lys Asn Ile Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Gly Pro Ser Phe Asp Ser Cys Leu Arg Asn Leu Glu Met
 165 170 175
 Val Leu Glx Arg Cys Val Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Arg Glu Gly Ile Val Leu Ser His Lys Ile Ser
 195 200 205
 Ala Arg Gly Ile Glu Val Asp Arg Ala Lys Ile Asp Val Ile Glu Lys
 210 215 220
 Leu Pro Pro Pro Leu Asn Ile Lys Gly Val Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 140

<211> 762

<212> DNA

<213> Glycine max

<400> 140

gtgcgcaagg aggtttttgaa gcttctagag gttgggctta tctaccccat ctccgacagc 60
 gcttgggtaa gccagtcctt ggtggtgtcg aagaaagagg gcatgacagt cattcgaaat 120
 gaaaagaatg acctgatacc aacacgaact gtcactagtt ggaaattatg catcgattac 180
 cgcaagctca acgaagccac aaggaaagac catttccctc tacccttcat ggatcagatg 240
 ttggagagac ttgcaggaca cgcttattat tgcttcttgg atgcatactt tggatataat 300
 cagattgttg tagaccccaa ggatcaggag aagatggcct tcacatgccc ttttgggtgc 360
 tttgcctata gacggattcc atttgggttg tgcaatgcac ctaccacatt ccaaattgtgc 420
 atgttggcca tttttgcaga tatagtggag aaaagcatcg aagtattcat ggatgacttt 480
 tcagtatttg tgccctcatt agaaagtgtt ttgaagaagt tggagatggg actacaaaga 540
 tgcgtgaaa caaacttagt actaaattgg gagaagtgtc acttcatggg tcgagaaggc 600
 atagtcttag gccataaaat ttgcaccga ggaattgagg tagaccaaac aaagattgat 660
 gtcattgaaa agttgccacc accatcaaat gttaaaggca tcaggagctt cctaggacaa 720
 gccaggttct acagaagatt catcaaggac ttcacaaaag tt 762

<210> 141

<211> 254

<212> PRT

<213> Glycine max

<400> 141

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	Glu	Val	Gly	Leu	Ile	Tyr	Pro
1				5					10					15	
Ile	Ser	Asp	Ser	Ala	Trp	Val	Ser	Pro	Val	Leu	Val	Val	Ser	Lys	Lys
			20					25					30		
Glu	Gly	Met	Thr	Val	Ile	Arg	Asn	Glu	Lys	Asn	Asp	Leu	Ile	Pro	Thr
		35					40				45				
Arg	Thr	Val	Thr	Ser	Trp	Lys	Leu	Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn
	50					55				60					
Glu	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Met	Asp	Gln	Met
65					70					75				80	
Leu	Glu	Arg	Leu	Ala	Gly	His	Ala	Tyr	Tyr	Cys	Phe	Leu	Asp	Ala	Tyr
			85					90						95	
Phe	Gly	Tyr	Asn	Gln	Ile	Val	Val	Asp	Pro	Lys	Asp	Gln	Glu	Lys	Met
			100					105					110		
Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val	Phe	Ala	Tyr	Arg	Arg	Ile	Pro	Phe
		115				120						125			
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Gln	Met	Cys	Met	Leu	Ala	Ile
	130					135					140				
Phe	Ala	Asp	Ile	Val	Glu	Lys	Ser	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155				160	
Ser	Val	Phe	Val	Pro	Ser	Leu	Glu	Ser	Cys	Leu	Lys	Lys	Leu	Glu	Met
				165					170					175	
Val	Leu	Gln	Arg	Cys	Val	Glu	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
			180					185					190		
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser
		195				200						205			
Thr	Arg	Gly	Ile	Glu	Val	Asp	Gln	Thr	Lys	Ile	Asp	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Ser	Asn	Val	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	Gln
225					230					235				240	
Ala	Arg	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
			245						250						

<210> 142

<211> 762

<212> DNA

<213> Glycine max

<400> 142

gtgcggaagg	aggttatttaa	gttgctagag	gcagggctca	tttaccta	ctcagatagt	60
tcatagggtta	gtcctgttca	tgttgctctg	aaaaagggag	gtatgacagt	gataaagaat	120
gatagagatg	agttaattcc	tacaagaata	gttactggat	ggaggatggg	tattgattac	180
aagaagctaa	atgaagccac	caggaaagac	cattaccgcg	ttcccttcat	ggatcaaagt	240
cttgagagac	ttgcagggca	atcttctctac	tattttattag	atggatactc	gggctacaat	300
caaattgcag	tggatcctca	ggaccaagaa	aagacagctt	tcacatgtcc	ttttgggtga	360
tttgcttatc	gccgcagtgc	gttcgggttta	tgtaatgccc	caactacttt	ccagagatgt	420
atgatggcaa	tttttgctga	catggtaaag	aaatgtattg	aagtttttat	ggacgatttc	480
tctgtctttg	gtgcattctt	tgaaaattgc	ctagcaaatt	tagagaaagt	gttacaacgc	540
tatgaagaat	ctaatttgg	gctcaactgg	gaaaaatgtc	actttatggt	tcaagaaggt	600
atcatgctgg	gacacaagat	ttctagaaga	ggaattaagg	tggataaggc	aaagattgag	660
gttattgata	aacttccacc	tctagttaat	gttagaggca	tacgaagttt	tttgggtcat	720
gctagattct	atcgatgatt	tatcaaggac	ttcaccaaag	tt		762

<210> 143

<211> 254
 <212> PRT
 <213> Glycine max

<400> 143

Val	Arg	Lys	Glu	Val	Ile	Lys	Leu	Leu	Glu	Ala	Gly	Leu	Ile	Tyr	Leu
1				5					10					15	
Ile	Ser	Asp	Ser	Ser	Glx	Val	Ser	Pro	Val	His	Val	Ala	Leu	Lys	Lys
		20						25					30		
Gly	Gly	Met	Thr	Val	Ile	Lys	Asn	Asp	Arg	Asp	Glu	Leu	Ile	Pro	Thr
		35					40					45			
Arg	Ile	Val	Thr	Gly	Trp	Arg	Met	Gly	Ile	Asp	Tyr	Lys	Lys	Leu	Asn
	50					55					60				
Glu	Ala	Thr	Arg	Lys	Asp	His	Tyr	Pro	Leu	Pro	Phe	Met	Asp	Gln	Met
65					70					75					80
Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ser	Ser	Tyr	Tyr	Leu	Leu	Asp	Gly	Tyr
				85					90					95	
Ser	Gly	Tyr	Asn	Gln	Ile	Ala	Val	Asp	Pro	Gln	Asp	Gln	Glu	Lys	Thr
			100					105					110		
Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val	Phe	Ala	Tyr	Arg	Arg	Met	Ser	Phe
		115					120					125			
Gly	Leu	Cys	Asn	Ala	Pro	Thr	Thr	Phe	Gln	Arg	Cys	Met	Met	Ala	Ile
	130					135					140				
Phe	Ala	Asp	Met	Val	Lys	Lys	Cys	Ile	Glu	Val	Phe	Met	Asp	Asp	Phe
145					150					155					160
Ser	Val	Phe	Gly	Ala	Ser	Phe	Glu	Asn	Cys	Leu	Ala	Asn	Leu	Glu	Lys
			165					170						175	
Val	Leu	Gln	Arg	Tyr	Glu	Glu	Ser	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys
		180						185					190		
Cys	His	Phe	Met	Val	Gln	Glu	Gly	Ile	Met	Leu	Gly	His	Lys	Ile	Ser
		195					200					205			
Arg	Arg	Gly	Ile	Lys	Val	Asp	Lys	Ala	Lys	Ile	Glu	Val	Ile	Asp	Lys
	210					215					220				
Leu	Pro	Pro	Leu	Val	Asn	Val	Arg	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His
225					230					235					240
Ala	Arg	Phe	Tyr	Arg	Glx	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 144
 <211> 761
 <212> DNA
 <213> Glycine max

<400> 144

gtg	cggaagg	aggtc	tttaa	gttg	ctggaa	gcagg	cctta	tttat	cccat	ttc	ggatagt	60
gcat	gggtta	gcc	ctatgca	agtt	gtccct	aagaa	aggag	gtat	gacagt	catta	aagaat	120
gataa	agatg	agtt	gatatc	caca	aggacc	gtc	accgggt	ggaga	atgtg	catt	gactat	180
cgaaa	gctga	atgat	gcacc	cgga	aggacc	attat	ccact	ccctt	tcatg	ggcc	atatgc	240
ttgaa	agact	tggtt	ggcaa	tcct	attatt	gtttt	ctaga	tggat	attat	ggtt	tataatc	300
agatt	gttgt	agat	cccaa	gat	caagaga	agac	agcttt	cacct	accct	ttt	ggtgtat	360
tcg	catatca	gtg	catgcct	ttt	ggtctat	gcaat	gcccc	agct	acattt	cag	aggtgta	420
tgat	ggctat	ttttt	ctgat	atgg	tggaaa	tatg	cattga	agttt	tcatg	gac	gatttct	480
ctatt	ttttg	gcc	atcctt	gaagg	gtgct	tat	caaact	tgaaa	aagta	ttaa	agagat	540
gtga	agagtc	caat	ctagtt	ctca	attgga	agaa	atgcc	ttt	catggt	caag	aaggaa	600
taat	gttggg	gcata	aaatt	tcag	taagag	ggat	agaggt	ggac	aaggca	aag	attgatg	660
taatt	gagaa	act	attgct	ccc	atgaatg	tca	aggggaat	aaga	agcttc	ttag	gacatg	720
cagg	gttcta	cagg	cgattc	ata	aaagact	tcac	caaagt	t				761

<210> 145
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 145
 Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ala Trp Val Ser Pro Met Gln Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile Lys Asn Asp Lys Asp Glu Leu Ile Ser Thr
 35 40 45
 Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
 50 55 60
 Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Gly His Met
 65 70 75 80
 Leu Glu Arg Leu Val Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Tyr Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Thr
 100 105 110
 Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Gln Cys Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Ala Ile
 130 135 140
 Phe Ser Asp Met Val Glu Ile Cys Ile Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Lys
 165 170 175
 Val Leu Lys Arg Cys Glu Glu Ser Asn Leu Val Leu Asn Trp Lys Lys
 180 185 190
 Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Ser
 195 200 205
 Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
 210 215 220
 Leu Leu Ala Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 146
 <211> 762
 <212> DNA
 <213> Glycine max

<400> 146
 gtgcgtaagg aggtgggtcaa gttgcttgaa gtaggactaa tttatccaat ctctgatagt 60
 gcttggtgta gttcgaacta ggtgggtgcct aagaaagggtg gtatgacggt gatccacaat 120
 gataagaatg atcttattcc tacacagaca atcattagggt ggcaaagtgtg tattgactat 180
 cacaagttga atgatgtcac caagaaggac cattttcctc tgccattcat ggaccaaagt 240
 ttagagagggt tagctggcca agctttttat tgttttttgg atggttattc tgggtataac 300
 caaatagcgg tgcattctta agatcaagag aagactacta tcatatgccc atttggtgtc 360
 tttgcttaca gacaaatgtc atttgaactg tgtaatgccc ctaccacctt ctagagattc 420
 atgatggcca tttttgctga cttgtggag aatgcatag aggtgttcat gaatgattc 480
 tctattttcg gctcttctt ttatcattgt ttatccaacc tggaattagt gttacaacgg 540
 tgtgcggaaa ccaatttgtt gatgaactgg gagaaatgtc atttcatggg ccaagagggg 600
 attgtcttag gccacaagat ctcttccaga ggggttgaag tggacaaggc aaaaattgat 660

gttattgaga agttgcctcc acctatgaat gtgaaaggca tccgaagttt tctcgaatat 720
 gttggatttt ataggagggtt catcaaagac ttcacgaaag tt 762

<210> 147
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 147
 Val Arg Lys Glu Val Val Lys Leu Leu Glu Val Gly Leu Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Ala Trp Val Ser Ser Asn Glx Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile His Asn Asp Lys Asn Asp Leu Ile Pro Thr
 35 40 45
 Gln Thr Ile Ile Arg Trp Gln Met Cys Ile Asp Tyr His Lys Leu Asn
 50 55 60
 Asp Val Thr Lys Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ala Gly Gln Ala Phe Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Ala Val His Leu Lys Asp Gln Glu Lys Thr
 100 105 110
 Thr Ile Ile Cys Pro Phe Gly Val Phe Ala Tyr Arg Gln Met Ser Phe
 115 120 125
 Glu Leu Cys Asn Ala Pro Thr Thr Phe Glx Arg Phe Met Met Ala Ile
 130 135 140
 Phe Ala Asp Leu Val Glu Lys Cys Ile Glu Val Phe Met Asn Asp Phe
 145 150 155 160
 Ser Ile Phe Gly Ser Ser Phe Tyr His Cys Leu Ser Asn Leu Glu Leu
 165 170 175
 Val Leu Gln Arg Cys Ala Glu Thr Asn Leu Leu Met Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
 195 200 205
 Ser Arg Gly Leu Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
 210 215 220
 Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Glu Tyr
 225 230 235 240
 Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 148
 <211> 762
 <212> DNA
 <213> Glycine max

<400> 148
 gtgcgtaagg aggttctcaa gcttttggag gttgggctca tatacctcat ctctgacagc 60
 gcttgggttaa gcctagtaca ggtggctccc aagaaatgcg gaatgacagt ggtacaaaat 120
 gagaggaatg acttgatacc aacacgaact gtcactggct agcggatgtg tatcgactac 180
 tgcaagttaga atgaagccac acggaaggac catttcccct tacctttcat ggatcagatg 240
 ctggagaggc ttgcagggca ggcatactac tgtttcttgg atagatatc aggatacaac 300
 caaatcgcg tagaccccag agatcaggag aagatggcct ttacatgccc ctttggcgtc 360
 tttgcttaca gaaggatgtc attcagggtta tgtaacgcac cagccacatt tcagaggtgc 420
 atgctggcca ttttttcaga catggtggag aagagcatcg aggtatttat ggatgaattc 480
 tcgatttttg gacccttatt tgacagttgc ttaaggaact tagagatggt actacagagg 540

tgcgatataga	ctaacttgggt	actaaattag	gaaaaatgtc	atttcattggt	tcgagagggga	600
atagtgatgg	gccacaatat	ctcagctaga	gggattgagg	ttgatcagac	aaagatagac	660
gtcattgaga	agttgccacc	accactgaat	gttaaaggcg	tcagaagttt	cttagggcat	720
gcaggtttct	acaggaggtt	cataaaagac	ttcacaaagg	tt		762

<210> 149
 <211> 254
 <212> PRT
 <213> Glycine max

<400> 149

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	Glu	Val	Gly	Leu	Ile	Tyr	Leu
1				5					10					15	
Ile	Ser	Asp	Ser	Ala	Trp	Val	Ser	Leu	Val	Gln	Val	Ala	Pro	Lys	Lys
			20					25					30		
Cys	Gly	Met	Thr	Val	Val	Gln	Asn	Glu	Arg	Asn	Asp	Leu	Ile	Pro	Thr
		35					40					45			
Arg	Thr	Val	Thr	Gly	Glx	Arg	Met	Cys	Ile	Asp	Tyr	Cys	Lys	Leu	Asn
	50					55					60				
Glu	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Met	Asp	Gln	Met
65					70					75				80	
Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ala	Tyr	Tyr	Cys	Phe	Leu	Asp	Arg	Tyr
				85					90					95	
Ser	Gly	Tyr	Asn	Gln	Ile	Ala	Val	Asp	Pro	Arg	Asp	Gln	Glu	Lys	Met
			100					105				110			
Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val	Phe	Ala	Tyr	Arg	Arg	Met	Ser	Phe
	115					120					125				
Arg	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Leu	Ala	Ile
	130					135					140				
Phe	Ser	Asp	Met	Val	Glu	Lys	Ser	Ile	Glu	Val	Phe	Met	Asp	Glu	Phe
145					150					155				160	
Ser	Ile	Phe	Gly	Pro	Leu	Phe	Asp	Ser	Cys	Leu	Arg	Asn	Leu	Glu	Met
			165					170					175		
Val	Leu	Gln	Arg	Cys	Val	Glx	Thr	Asn	Leu	Val	Leu	Asn	Glx	Glu	Lys
		180						185					190		
Cys	His	Phe	Met	Val	Arg	Glu	Gly	Ile	Val	Met	Gly	His	Asn	Ile	Ser
	195						200					205			
Ala	Arg	Gly	Ile	Glu	Val	Asp	Gln	Thr	Lys	Ile	Asp	Val	Ile	Glu	Lys
	210					215					220				
Leu	Pro	Pro	Pro	Leu	Asn	Val	Lys	Gly	Val	Arg	Ser	Phe	Leu	Gly	His
225					230					235				240	
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val		
				245					250						

<210> 150
 <211> 761
 <212> DNA
 <213> Glycine max

<400> 150

gtgcgtaagg	agggttttta	gttgctggaa	gcaggctctta	tttatcccat	ttcggatagt	60
gcatgggtta	gccctgtgca	ggttgtcccc	aagaaagaag	gtaagacagt	cattaaggat	120
gaaaaggatg	agttgatatc	cacaaggact	atcaccgggt	ggagaatgtg	cattgactat	180
cagaagctga	atgatgccac	ccggaaggac	cattatccac	tccctttcat	ggaccaaag	240
cttgaaagac	ttgccgggca	atcttattat	tgttttctgg	atggatattc	tggttataat	300
cagattgatg	tagatcccaa	ggatcaagag	aagactgctt	tcacctaccc	ttttggtgta	360
ttcgccctatc	ggcgcatgcc	ctttggtttg	tgcaatgccc	cagctacatt	tcagaggtgt	420

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atgatgacta ttttttctga tatggtggaa aaatgaattg aagttttcat ggacgatttc 480
tctatttttg ggccatcttt tgaagggtgc ttatcaaadc ttgaaagagt attaaagaga 540
cgtgaagagt ccaaactagt tctcaattgg gagaaatgcc atttcatggg tcaagaagga 600
atagtgtggg gcataaaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660
taatagagaa actacctcct cccatgaatg tcaaggggaat aagaagcttc ctaggacatg 720
caggggttcta caagcgattc atcaaagatt tcacaaaggt t 761

```

<210> 151

<211> 254

<212> PRT

<213> Glycine max

<400> 151

```

Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
1      5      10      15
Ile Ser Asp Ser Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
20      25      30
Glu Gly Lys Thr Val Ile Lys Asp Glu Lys Asp Glu Leu Ile Ser Thr
35      40      45
Arg Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
50      55      60
Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
65      70      75      80
Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
85      90      95
Ser Gly Tyr Asn Gln Ile Asp Val Asp Pro Lys Asp Gln Glu Lys Thr
100     105     110
Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
115     120     125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Thr Ile
130     135     140
Phe Ser Asp Met Val Glu Lys Glx Ile Glu Val Phe Met Asp Asp Phe
145     150     155     160
Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Arg
165     170     175
Val Leu Lys Arg Arg Glu Glu Ser Lys Leu Val Leu Asn Trp Glu Lys
180     185     190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
195     200     205
Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
210     215     220
Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
225     230     235     240
Ala Gly Phe Tyr Lys Arg Phe Ile Lys Asp Phe Thr Lys Val
245     250

```

<210> 152

<211> 762

<212> DNA

<213> Glycine max

<400> 152

```

gtgcggaag aggtattcaa gttactagag gcagggtc tctacccaat ttcagatagc 60
tcctgggtta gtccggttca agttgttcca aaaaaaggag ggatgacagt ggtaaaaaat 120
gatagaaatg agctaattcc tacaagaaga gtcaccagat ggagaatgtg tattgattat 180
aggaagctca atgaagccac aagaaaagac cattaccac ttcccttcat ggatcaaatg 240
cttaagagac ttgcaaggca atccttctac cgtttcttgg acggatactc aggttacaat 300

```

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cagattgcag tggatcctca ggatcaagaa aaaacagctt ttacatgtcc tttcagtgtt 360
tttgcttata gccgcatgcc gttcgggtta tgtaatgcct ctactacttt tcagagatgt 420
atgatggcaa tttttgatga catggttagag aaatgtattg aagtctttat ggatgatttt 480
tcgttctttg gtgcatcttt tggaaattgc ttagcaaatt tagagaaagt gttacaacgt 540
tgtgaaaaat ctaatttggt gcttaactgg gaaaaatgtc actttatggt acaagaaggt 600
attgtgctag gacacaaaat ctctaaaaga ggaattgagg tggttaaaaga aaaactagat 660
gttattgata aacttccacc cccagttaat gtaaaaggca tacacagttt tttgggtcat 720
gttgattttt atcggcgatt cataaaggac ttcaccaaag tt 762

```

<210> 153
 <211> 254
 <212> PRT
 <213> Glycine max

```

<400> 153
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
1          5          10          15
Ile Ser Asp Ser Ser Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
20          25          30
Gly Gly Met Thr Val Val Lys Asn Asp Arg Asn Glu Leu Ile Pro Thr
35          40          45
Arg Arg Val Thr Arg Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
50          55          60
Glu Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
65          70          75          80
Leu Lys Arg Leu Ala Arg Gln Ser Phe Tyr Arg Phe Leu Asp Gly Tyr
85          90          95
Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Gln Asp Gln Glu Lys Thr
100          105          110
Ala Phe Thr Cys Pro Phe Ser Val Phe Ala Tyr Arg Arg Met Pro Phe
115          120          125
Gly Leu Cys Asn Ala Ser Thr Thr Phe Gln Arg Cys Met Met Ala Ile
130          135          140
Phe Asp Asp Met Val Glu Lys Cys Ile Glu Val Phe Met Asp Asp Phe
145          150          155          160
Ser Phe Phe Gly Ala Ser Phe Gly Asn Cys Leu Ala Asn Leu Glu Lys
165          170          175
Val Leu Gln Arg Cys Glu Lys Ser Asn Leu Val Leu Asn Trp Glu Lys
180          185          190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
195          200          205
Lys Arg Gly Ile Glu Val Val Lys Glu Lys Leu Asp Val Ile Asp Lys
210          215          220
Leu Pro Pro Pro Val Asn Val Lys Gly Ile His Ser Phe Leu Gly His
225          230          235          240
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
245          250

```

<210> 154
 <211> 761
 <212> DNA
 <213> Glycine max

```

<400> 154
gtgcgtaaaag aagtttttgaa gctgctagaa gcagacctta tttatcccat ttcggatagt 60
acatgggtta gccctgtgca agttgtcccc gagaaaggag gtatgacagt cattaagaat 120
gataaagatg agttgatatc cacaaggact gtcaccgggt gagaatgtgc attgactatc 180

```

```

ggaagctgaa tgatgccacc cagaaggacc attattcact ccctttcatg gaccagatgc 240
ttgaaagact tgccggacaa tcctattatt gttttctgaa tggatactct ggctataatc 300
agattgtggt agatcccaaa gatcaggaga aaactgcttt cacctgcctt tttgggtgat 360
ttgcatacaa gcgtatgcat tttggcttgt gtaatgctcc aactacgtgt cagaggtgta 420
tgatgactat tttttctggt atcgtggaaa aatgcattga acttttcatg gacgatttct 480
ctatttttgg gccatctttt gaaggctact tatcaaacct tgaaagagta ttacagagat 540
gtgaagagtc taatctagtt ctcaattggg agaaatgcc tttcatgggt caagaaggaa 600
tagtgctggg gcataaaatt tcagtaagag ggatagaggt ggacaaggca aagattgatg 660
taattgagaa actacctcct cccatgattg tcaagggaat aagaagcctc ctaggacatg 720
tagggttcta caggcgattc atcaaagact tcacaaaggt t 761

```

<210> 155

<211> 254

<212> PRT

<213> Glycine max

<400> 155

```

Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Asp Leu Ile Tyr Pro
 1          5          10          15
Ile Ser Asp Ser Thr Trp Val Ser Pro Val Gln Val Val Pro Glu Lys
          20          25          30
Gly Gly Met Thr Val Ile Lys Asn Asp Lys Asp Glu Leu Ile Ser Thr
          35          40          45
Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
          50          55          60
Asp Ala Thr Gln Lys Asp His Tyr Ser Leu Pro Phe Met Asp Gln Met
65          70          75          80
Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asn Gly Tyr
          85          90          95
Ser Gly Tyr Asn Gln Ile Val Val Asp Pro Lys Asp Gln Glu Lys Thr
          100          105          110
Ala Phe Thr Cys Leu Phe Gly Val Phe Ala Tyr Lys Arg Met His Phe
          115          120          125
Gly Leu Cys Asn Ala Pro Thr Thr Cys Gln Arg Cys Met Met Thr Ile
          130          135          140
Phe Ser Gly Ile Val Glu Lys Cys Ile Glu Leu Phe Met Asp Asp Phe
145          150          155          160
Ser Ile Phe Gly Pro Ser Phe Glu Gly Tyr Leu Ser Asn Leu Glu Arg
          165          170          175
Val Leu Gln Arg Cys Glu Glu Ser Asn Leu Val Leu Asn Trp Glu Lys
          180          185          190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
          195          200          205
Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
210          215          220
Leu Pro Pro Pro Met Ile Val Lys Gly Ile Arg Ser Leu Leu Gly His
225          230          235          240
Val Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
          245          250

```

<210> 156

<211> 762

<212> DNA

<213> Glycine max

<400> 156

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gtgcgtaagg aggttttttaa gttgctggaa gcaggtctta tttatcccat ttcggatagt

```

60

```

gcatggggtta gccctgtgca ggttggtcccc aagaaagaag gtaagacagt cattaaggat 120
gaaaaagatg agttgatatc cacaaggact atcacggggt ggagaatgtg cattgactat 180
cagaagctga atgatgccac ccggaaggac cattatccac tccctttcat ggaccaaagtg 240
cttgaaagac ttgccgggca atcttattat tgttttctgg atggatattc tgggtataat 300
cagattgatg tagatcccaa ggatcaagag aagactgctt tcacctaccc ttttgggtga 360
ttcgccctatc ggccgatgcc ctttggtttg tgcaatgccc cagctacatt tcagaggtgt 420
atgatgacta ttttttctga tatggtggaa aaatgaattg aagttttcat ggacgatgtc 480
tctatttttg ggccatcttt tgaagggtgc ttatcaaadc ttgaaagagt attaaagaga 540
cgtgaagagt ccaaactagt tctcaattgg gagaaatgcc atttcatggt tcaagaagga 600
atagtgttgg ggcataaaat ttcagtaaga gggatagagg tggacaaggc aaagattgat 660
gtaatagaga aactacctcc tcccatgaat gtcaagggaa taagaagctt cctaggacat 720
gcagggttct acaagcgatt catcaaagac ttctcaaaag tt 762

```

<210> 157
 <211> 254
 <212> PRT
 <213> Glycine max

```

<400> 157
Val Arg Lys Glu Val Phe Lys Leu Leu Glu Ala Gly Leu Ile Tyr Pro
 1           5           10           15
Ile Ser Asp Ser Ala Trp Val Ser Pro Val Gln Val Val Pro Lys Lys
      20           25           30
Glu Gly Lys Thr Val Ile Lys Asp Glu Lys Asp Glu Leu Ile Ser Thr
      35           40           45
Arg Thr Ile Thr Gly Trp Arg Met Cys Ile Asp Tyr Gln Lys Leu Asn
      50           55           60
Asp Ala Thr Arg Lys Asp His Tyr Pro Leu Pro Phe Met Asp Gln Met
      65           70           75           80
Leu Glu Arg Leu Ala Gly Gln Ser Tyr Tyr Cys Phe Leu Asp Gly Tyr
      85           90           95
Ser Gly Tyr Asn Gln Ile Asp Val Asp Pro Lys Asp Gln Glu Lys Thr
      100          105          110
Ala Phe Thr Tyr Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
      115          120          125
Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Met Met Thr Ile
      130          135          140
Phe Ser Asp Met Val Glu Lys Glx Ile Glu Val Phe Met Asp Asp Val
      145          150          155          160
Ser Ile Phe Gly Pro Ser Phe Glu Gly Cys Leu Ser Asn Leu Glu Arg
      165          170          175
Val Leu Lys Arg Arg Glu Glu Ser Lys Leu Val Leu Asn Trp Glu Lys
      180          185          190
Cys His Phe Met Val Gln Glu Gly Ile Val Leu Gly His Lys Ile Ser
      195          200          205
Val Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
      210          215          220
Leu Pro Pro Pro Met Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
      225          230          235          240
Ala Gly Phe Tyr Lys Arg Phe Ile Lys Asp Phe Ser Lys Val
      245          250

```

<210> 158
 <211> 761
 <212> DNA
 <213> Glycine max

<400> 158

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gtgcggaagg aggttcttaa gtcctggaa gcagggctca tctatcttat ctcagatagt      60
gttgggtgag tccagtgcag gtgggtccca agaaggggtg gaagactgtg gtgagaaatg      120
agaaaaatga cctcattcta acccgaactg tcacaggatg gagaatgtgc atagattatc      180
ggaagttgaa tgatgccatc aagaaggatc acttccctct accattcata gatcagatgc      240
ttgagagggt agcaagccag tctttctatt atttcttgga tgaatattct agatacaatc      300
agattgctat acatcccaag gaccaagaga agattgcatt tacatgcca tttggtgtct      360
ttgcctatag aaggatgcca tttgaactat gcaatgctcc agctaccttt tagaggcata      420
tgctagccat attcgctaac atgggtggaga aatgcatcga agtggtcata gatgattttt      480
cgggtgttgg tccatccttt gtttgttgtt tgaccaatth agagctagtg ttgaagtact      540
gtgaggagac aaatttagta ttgaattggg agaaatgtca tttcatggtc caagaaggaa      600
ttatgttggg gcataaaatt tttgctagag gtattgaggt ggacaaggcc aaaattgatg      660
ttattgaaaa gctgcctcca ccagtcaatg taaaaggcat caggagtttt cttggacaca      720
ctggtttctt caggcgtttc atcaaggact tcacaaaagt t                        761

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<210> 159

<211> 254

<212> PRT

<213> Glycine max

<400> 159

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Val Arg Lys Glu Val Leu Lys Leu Leu Glu Ala Gly Leu Ile Tyr Leu
  1           5           10           15
Ile Ser Asp Ser Ala Trp Val Ser Pro Val His Val Val Pro Lys Lys
      20           25           30
Gly Gly Lys Thr Val Val Arg Asn Glu Lys Asn Asp Leu Ile Leu Thr
      35           40           45
Arg Thr Val Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Lys Leu Asn
      50           55           60
Asp Ala Ile Lys Lys Asp His Phe Pro Leu Pro Phe Ile Asp Gln Met
      65           70           75           80
Leu Glu Arg Leu Ala Ser Gln Ser Phe Tyr Tyr Phe Leu Asp Glu Tyr
      85           90           95
Ser Arg Tyr Asn Gln Ile Ala Ile His Pro Lys Asp Gln Glu Lys Ile
      100          105          110
Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Arg Met Pro Phe
      115          120          125
Glu Leu Cys Asn Ala Pro Ala Thr Phe Glx Arg His Met Leu Ala Ile
      130          135          140
Phe Ala Asn Met Val Glu Lys Cys Ile Glu Val Phe Ile Asp Asp Phe
      145          150          155          160
Ser Val Phe Gly Pro Ser Phe Val Cys Cys Leu Thr Asn Leu Glu Leu
      165          170          175
Val Leu Lys Tyr Cys Glu Glu Thr Asn Leu Val Leu Asn Trp Glu Lys
      180          185          190
Cys His Phe Met Val Gln Glu Gly Ile Met Leu Gly His Lys Ile Phe
      195          200          205
Ala Arg Gly Ile Glu Val Asp Lys Ala Lys Ile Asp Val Ile Glu Lys
      210          215          220
Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
      225          230          235          240
Thr Gly Phe Phe Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
      245          250

```

<210> 160

<211> 762

<212> DNA

<213> Pisum sativum

<400> 160

gtg	cgcaagg	aagtactcaa	gttg	tttagat	tcgggaatga	ttt	accccat	ttctgacagc	60
tcgt	gggtaa	gtccagtgca	cgtg	gtacca	aagaaaggag	gaacctcagt	aattttaaat		120
gaaa	agaatg	aactgatccc	aactcgcaca	gtgacagggt	ggcgagtatg	catcgatcac			180
agaagactga	acacagcaac	aagaaaggat	cattttcctc	tcccttttat	tgatcaa	aatg			240
ttagaaagac	ttgcagggtca	tgagtattat	tgctttctgg	atggatattc	gggatacaat				300
caaattgttg	tagccccgga	agatcaggaa	aaaactgcat	ttacatgtcc	ttatggtatt				360
ttcgtttaca	gacggatgcc	atttgggcta	tgcaatgccc	cagctacttt	tcagagggtgt				420
atgacatcta	tattctccga	catgcttgaa	aagtatatga	aggtgtttat	ggatgatttc				480
tctgtgtttg	gttcttcttt	tgataattgt	ttagctaact	tgtctcttgt	tttgcaaaga				540
tgtcaggaaa	ctaaccttgt	tctcaattgg	gagaaatgtc	atttcatggt	gcaggaagga				600
attgtgctag	gacacaaaat	ttcccacaaa	ggaattgaag	tggacaaagc	caaagtggag				660
gttatagcta	acctcccacc	tccggtgaat	gaaaaaggga	taaggagttt	tttgggtcat				720
gcagggtttt	atcgcagggt	catcaaagac	ttcaciaaag	tt					762

<210> 161

<211> 254

<212> PRT

<213> Pisum sativum

<400> 161

Val	Arg	Lys	Glu	Val	Leu	Lys	Leu	Leu	Asp	Ser	Gly	Met	Ile	Tyr	Pro	
1				5					10						15	
Ile	Ser	Asp	Ser	Ser	Trp	Val	Ser	Pro	Val	His	Val	Val	Pro	Lys	Lys	
			20					25					30			
Gly	Gly	Thr	Ser	Val	Ile	Leu	Asn	Glu	Lys	Asn	Glu	Leu	Ile	Pro	Thr	
		35					40					45				
Arg	Thr	Val	Thr	Gly	Trp	Arg	Val	Cys	Ile	Asp	His	Arg	Arg	Leu	Asn	
	50					55					60					
Thr	Ala	Thr	Arg	Lys	Asp	His	Phe	Pro	Leu	Pro	Phe	Ile	Asp	Gln	Met	
65					70					75					80	
Leu	Glu	Arg	Leu	Ala	Gly	His	Glu	Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr	
			85					90						95		
Ser	Gly	Tyr	Asn	Gln	Ile	Val	Val	Ala	Pro	Glu	Asp	Gln	Glu	Lys	Thr	
			100					105					110			
Ala	Phe	Thr	Cys	Pro	Tyr	Gly	Ile	Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe	
		115					120					125				
Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr	Phe	Gln	Arg	Cys	Met	Thr	Ser	Ile	
	130					135					140					
Phe	Ser	Asp	Met	Leu	Glu	Lys	Tyr	Met	Lys	Val	Phe	Met	Asp	Asp	Phe	
145				150						155					160	
Ser	Val	Phe	Gly	Ser	Ser	Phe	Asp	Asn	Cys	Leu	Ala	Asn	Leu	Ser	Leu	
			165					170					175			
Val	Leu	Gln	Arg	Cys	Gln	Glu	Thr	Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	
		180						185					190			
Cys	His	Phe	Met	Val	Gln	Glu	Gly	Ile	Val	Leu	Gly	His	Lys	Ile	Ser	
	195						200					205				
His	Lys	Gly	Ile	Glu	Val	Asp	Lys	Ala	Lys	Val	Glu	Val	Ile	Ala	Asn	
	210				215						220					
Leu	Pro	Pro	Pro	Val	Asn	Glu	Lys	Gly	Ile	Arg	Ser	Phe	Leu	Gly	His	
225				230						235					240	
Ala	Gly	Phe	Tyr	Arg	Arg	Phe	Ile	Lys	Asp	Phe	Thr	Lys	Val			
			245					250								

<210> 162

<211> 762
 <212> DNA
 <213> Pisum sativum

<400> 162
 gtgcgtaagg aggtctttaa actattggat gcgggaatga tttacccgat ctccgatatgt 60
 ccgtgggtta gtcccggtgca cgtgggtccg aagaagggtg gaatgaccgt aatccgtaat 120
 gacaaagacg aattgatccc gactaaagtt gcaacggggt ggagaatatg tatagattat 180
 agacagttga ataccgcgac tcgaaaggac cattttccac tcccatttat ggatcaaatg 240
 cttgaaagac tatcggggcca acaatactat tgtttcttgg acggctactc cgggtacaac 300
 caaattgcgg ttgaccgggt tgatcatgag aagacggctt tcacgtgtcc gtttggagtg 360
 ttgcataca gaaaaatgcc ctttgggctg tgcaatgcac cggcgacttt ccaacgatgc 420
 gtccatagcca tttttgccga tctaataagag aaaacaatgg acgtcttcat ggatgacttc 480
 tcgggtatttg gtgggacggt tagtctatgc ttggcaaatt tgaagacggt gttggaaagg 540
 tgtgtgaaga ccaatttgggt gctaaattgg gaaaagtgtc acttcatggt gaccgagggg 600
 atcgtgctag gccacaaagt ctctaaaagg gggcttgaag tggatagagc taaggttgaa 660
 gtaattgaaa aattaccccc tccggtgaat gtgaaaggca tccgtagctt tttggggcac 720
 gcgggggttt accggcgctt cattaaagac ttctcaaaag tt 762

<210> 163
 <211> 254
 <212> PRT
 <213> Pisum sativum

<400> 163
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Met Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Pro Trp Val Ser Pro Val His Val Val Pro Lys Lys
 20 25 30
 Gly Gly Met Thr Val Ile Arg Asn Asp Lys Asp Glu Leu Ile Pro Thr
 35 40 45
 Lys Val Ala Thr Gly Trp Arg Ile Cys Ile Asp Tyr Arg Gln Leu Asn
 50 55 60
 Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ser Gly Gln Gln Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Val Asp His Glu Lys Thr
 100 105 110
 Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Lys Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Leu Ala Ile
 130 135 140
 Phe Ala Asp Leu Ile Glu Lys Thr Met Asp Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Gly Gly Thr Phe Ser Leu Cys Leu Ala Asn Leu Lys Thr
 165 170 175
 Val Leu Glu Arg Cys Val Lys Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Thr Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Lys Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys
 210 215 220
 Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240
 Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Ser Lys Val
 245 250

<210> 164
 <211> 762
 <212> DNA
 <213> Pisum sativum

<400> 164
 gtgcggaagg aggtctttaa attgttggat gcggggatga tttacccgat ctcggatagt 60
 ccatgggtta gtcctgtgca cgttgttccg aagaaggggg ggattaccgt aatccggaat 120
 gacaaggatg aattgatccc cactaaagtt gaaacggggg ggagaatgtg tattgattat 180
 aggcggttga ataccgcgac tcgaaaagac cattttccac tcccatttat ggatcaaata 240
 ctcgaaagac tatcgggcca acaatattat tgttttttgg acggctactc cgggtacaac 300
 caaattgcgg ttgacccggc cgatcatgag aagacggctt tcacatgtcc gtttggagtg 360
 ttgcataacc gaaaaatgcc ctttgggctg tgcaatgcac cggcgacctt ccaacgatgt 420
 gtccaagcca tttttgtcga tctgatagag aaaacaatgg aagtcttcat ggatgacttc 480
 tcggtatttg gtgggtcttt tagtctatgc ttggcgaaact tgaaaacggg gttggagaga 540
 tgtgtgaaga ccaatttggt gcttaattgg gagaagtgtc acttcatggg gaccgagggg 600
 atcgtgctag gccacaaagt ctctagaagg gggcttgaag tggatagagc taagggtgaa 660
 gtgatagaaa aattacctcc tccggtgaat gtgaagggca tccgaagctt tttggggcac 720
 gccgggttct accggcgctt cattaaagat ttcacaaagg tt 762

<210> 165
 <211> 254
 <212> PRT
 <213> Pisum sativum

<400> 165
 Val Arg Lys Glu Val Phe Lys Leu Leu Asp Ala Gly Met Ile Tyr Pro
 1 5 10 15
 Ile Ser Asp Ser Pro Trp Val Ser Pro Val His Val Val Pro Lys Lys
 20 25 30
 Gly Gly Ile Thr Val Ile Arg Asn Asp Lys Asp Glu Leu Ile Pro Thr
 35 40 45
 Lys Val Glu Thr Gly Trp Arg Met Cys Ile Asp Tyr Arg Arg Leu Asn
 50 55 60
 Thr Ala Thr Arg Lys Asp His Phe Pro Leu Pro Phe Met Asp Gln Met
 65 70 75 80
 Leu Glu Arg Leu Ser Gly Gln Gln Tyr Tyr Cys Phe Leu Asp Gly Tyr
 85 90 95
 Ser Gly Tyr Asn Gln Ile Ala Val Asp Pro Ala Asp His Glu Lys Thr
 100 105 110
 Ala Phe Thr Cys Pro Phe Gly Val Phe Ala Tyr Arg Lys Met Pro Phe
 115 120 125
 Gly Leu Cys Asn Ala Pro Ala Thr Phe Gln Arg Cys Val Gln Ala Ile
 130 135 140
 Phe Val Asp Leu Ile Glu Lys Thr Met Glu Val Phe Met Asp Asp Phe
 145 150 155 160
 Ser Val Phe Gly Gly Ser Phe Ser Leu Cys Leu Ala Asn Leu Lys Thr
 165 170 175
 Val Leu Glu Arg Cys Val Lys Thr Asn Leu Val Leu Asn Trp Glu Lys
 180 185 190
 Cys His Phe Met Val Thr Glu Gly Ile Val Leu Gly His Lys Val Ser
 195 200 205
 Arg Arg Gly Leu Glu Val Asp Arg Ala Lys Val Glu Val Ile Glu Lys
 210 215 220
 Leu Pro Pro Pro Val Asn Val Lys Gly Ile Arg Ser Phe Leu Gly His
 225 230 235 240

Ala Gly Phe Tyr Arg Arg Phe Ile Lys Asp Phe Thr Lys Val
 245 250

<210> 166
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated oligonucleotide

<221> misc_feature
 <222> 6, 15, 16, 18
 <223> n = A,T,C or G

<400> 166
 gtgcgnaarg argtnntnaa ryt

23

<210> 167
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 167
 Val Arg Lys Glu Val Leu Lys Leu
 1 5

<210> 168
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetically generated oligonucleotide

<221> misc_feature
 <222> 7
 <223> n = A,T,C or G

<400> 168
 aacyttngwr aartcyttta traa

24

<210> 169
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> plant retroelement sequence

<400> 169
 Val Lys Ser Phe Asp Lys Ile Phe
 1 5

<210> 170
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 170
 gggatccgca attagaatct 20

<210> 171
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 171
 cgaattcggg ccacttcgga 20

<210> 172
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 172
 ccacaagatt ctaattgcgg attc 24

<210> 173
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 173
 ccgaaatgga ccgaacccga catc 24

<210> 174
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 174
 tttccaggct cttgacgaga ttg 24

<210> 175
 <211> 22

<212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 175
 cgactcgagc tccatagcga tg 22

<210> 176
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 176
 cggattgggc cgaaatggac cgaa 24

<210> 177
 <211> 18
 <212> DNA
 <213> Arabidopsis thaliana

<400> 177
 gaggacttgg ggggcaaa 18

<210> 178
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<221> VARIANT
 <222> 2-3, 5-7, 9-12
 <223> Xaa = Any Amino Acid

<400> 178
 Cys Xaa Xaa Cys Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Cys
 1 5 10

<210> 179
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<400> 179
 Leu Ile Asp Leu Gly Ala
 1 5

<210> 180

<211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<400> 180
 Lys Thr Ala Phe
 1

<210> 181
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> 2
 <223> Xaa = Pro or Ser

<400> 181
 Met Xaa Phe Gly Leu Cys Asn Ala
 1 5

<210> 182
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> 1
 <223> Xaa = Val, Ile, or Met

<221> VARIANT
 <222> 9
 <223> Xaa = Ser or Trp

<221> VARIANT
 <222> 10
 <223> Xaa = Val or Ile

<400> 182
 Xaa Glu Val Phe Met Asp Asp Phe Xaa Xaa
 1 5 10

<210> 183
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 12

<223> Xaa = Ile or Val

<400> 183

Phe	Glu	Leu	Met	Cys	Asp	Ala	Ser	Asp	Tyr	Ala	Xaa	Gly	Ala	Val	Leu
1				5					10					15	
Gly	Gln	Arg													

<210> 184

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 4

<223> Xaa = Thr or Ile

<221> VARIANT

<222> 8

<223> Xaa = Leu or Met

<221> VARIANT

<222> 13

<223> Xaa = Phe or Tyr

<221> VARIANT

<222> 15

<223> Xaa = Leu or Phe

<221> VARIANT

<222> 19

<223> Xaa = Arg or Lys

<221> VARIANT

<222> 23

<223> Xaa = Ile or Val

<221> VARIANT

<222> 26

<223> Xaa = Arg or Lys

<400> 184

Tyr	Ala	Thr	Xaa	Glu	Lys	Glu	Xaa	Leu	Ala	Ile	Val	Xaa	Ala	Xaa	Glu
1				5					10					15	
Lys	Phe	Xaa	Ser	Tyr	Leu	Xaa	Gly	Ser	Xaa	Val					
			20					25							

<210> 185

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 4, 6-7, 11-40, 43

<223> Xaa = Any Amino Acid

<400> 185

His	Cys	His	Xaa	Ser	Xaa	Xaa	Gly	Gly	His	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Asp	Xaa	Cys	Gln	Arg		
			35				40						45		

<210> 186

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 6

<223> Xaa = Ile, Val, or Met

<400> 186

Trp	Gly	Ile	Asp	Phe	Xaa	Gly	Pro
1				5			

<210> 187

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 7

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> 10

<223> Xaa = Ala or Val

<400> 187

Pro	Tyr	His	Pro	Gln	Thr	Xaa	Gly	Gln	Xaa	Glu
1				5					10	

<210> 188

<211> 13

<212> DNA

<213> Artificial Sequence

<220>
 <223> consensus sequence

<221> misc_feature
 <222> 11, 12
 <223> n = A,T,C or G

<400> 188
 atttgggggra nnt

13

<210> 189
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> 5, 8
 <223> Xaa = Arg or Lys

<400> 189
 Gln Met Ala Ser Xaa Lys Arg Xaa Ala
 1 5

<210> 190
 <211> 6
 <212> PRT
 <213> Pisum sativum

<400> 190
 Ala Ser Lys Lys Arg Lys
 1 5

CI
 Conew